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Perfect score:
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Listing first 45 summaries
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                                                                                                                                                                                                                                                                                  Result
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*

7: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

8: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

9: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

9: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
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'Cgn2_6/ptodata/11/pubpaa/US09C_PUBCOMB.pep:*
'Cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
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'Cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
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12 US-9-287-849-22

12 US-10-359-460-22

12 US-10-098-732A-18

12 US-10-098-732A-18

12 US-10-098-732A-65

12 US-10-359-460-2

13 US-10-098-732A-16

14 US-10-098-732A-16

15 US-10-098-732A-16

17 US-10-193-002-106
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US-09-287-849-26
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US-10-193-002-102
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 Sequence 107, App
Sequence 12, Appl
Sequence 26, Appl
Sequence 26, Appl
Sequence 26, Appl
Sequence 27, Appl
Sequence 22, Appl
Sequence 22, Appl
Sequence 12, Appl
Sequence 12, Appl
Sequence 15, Appl
Sequence 16, Appl
Sequence 16, Appl
Sequence 16, Appl
Sequence 16, Appl
Sequence 11, App
Sequence 111, App
Sequence 111, App
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## ALIGNMENTS

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US-10-084-843-107
Sequence 107, Application US/10084843
Sequence 107, Application US/10084843
Publication No. US20030143243A1
GENERAL INFORMATION:
Skeiky, Yasir A.W.
Dillon, Davin C.
Campos-Neto, Antonio
Houghton, Raymond
Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
Lodes, Michael J.
Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
NUMBER OF SEQUENCES: 355
CORRESPONDENCE ADDRESS:
ADDRESS: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER PAPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION UNMBER: US/10/084,843
FILING DATE: 25-Feb-2002
CLASSIFICATION: CUNKnown>
PRIOR APPLICATION UNMBER: US/10/084,843
FILING DATE: 05-MAY-1998
ATTORNEY, AGENT INFORMATION:
NAME: Maki, David J.
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RESULT 2
US-10-193-002-102
; Sequence 102, Applicati
; Publication No. US20030
; Publication No. US20030
; GENERAL INFORMATION:
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SEQUENCE CHARACTERISTICS:
LENGTH: 391 amino acids
TYPE: amino acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE DESCRIPTION: SEQ ID NO: 107:
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center,
                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                   TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GOMGARAGGGLSGVLRVPPRPYVMPHSPAAG
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                                                                                  CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Application US/10193002 o. US20030135026A1
                                                                                                                                                                                                                                                      Houghton, Raymond
Vedvick, Thomas S.
Vedvick, Daniel R.
Twardzik, Daniel R.
Lodes, Michael J.
Hendrickson, Ronald C.
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Dillon, Davin C.
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Pred. No. 7.1e-146;
; Mismatches 0;
                                                                                                                                   701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            391
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        GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Skeiky, Yasir

APPLICANT: Skeiky, Yasir

APPLICANT: Guderian, Mark

APPLICANT: Corixa Corporation

TITLE OF INVENTION: Heterologous Fusion Protein Constructs Comprising

TITLE OF INVENTION: Leishmania Antigen

FILE REFERENCE: 014058-012010US

CURRENT APPLICATION UNMERER: US/10/098,732A

CURRENT FILING DATE: 2003-04-29
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                                                                                                                                                                                                                       Sequence 14, Application US/10098732A Publication No. US20030175294A1
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SEQUENCE CHARACTERISTICS:
LENGTH: 391 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
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NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-WAY-1998
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Pred. No. 7.1e-146;
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TITLE OF INVENTION: Pusion Protiens of Mycobacterium tuberculosis Antigens TITLE OF INVENTION: And Their Uses FILE REFERENCE: 014058-009020US CURRENT APPLICATION NUMBER: US/09/287,849 CURRENT FILING DATE: 1999-04-07 PRIOR APPLICATION NUMBER: US 08/818,112 PRIOR FILING DATE: 1997-03-13 PRIOR APPLICATION NUMBER: US 08/942,578 PRIOR APPLICATION NUMBER: US 08/942,578 PRIOR APPLICATION NUMBER: US 09/025,197 PRIOR PILING DATE: 1997-10-01 PRIOR PILING DATE: 1998-02-18 PRIOR APPLICATION NUMBER: US 09/025,197 PRIOR APPLICATION NUMBER: US 09/056,556 PRIOR PILING DATE: 1998-02-10 PRIOR PILING DATE: 1998-02-30 NUMBER: US 09/223,040 PRIOR PILING DATE: 1998-12-30 NUMBER: US 09/223,040
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; PRIOR APPLICATION NUMBER: US 60; PRIOR FILING DATE: 2001-03-13; NUMBER OF SEQ ID NOS: 80; SOFTWARE: PatentIn Ver. 2.1; SEQ ID NO 14; LENGTH: 391
                                                                                                                                                                                                                                                                                                                                APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Alderson, Mark
APPLICANT: Campos-Neto, Antonio
APPLICANT: Corixa Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 26, Application US/09287849 Patent No. US20020009459A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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ORGANISM: Mycobacterium tuberculosis
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Campos-Neto, Antonio
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RESULT 5
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                                                                           GENERAL INFORMATION:
                                                                                           Sequence 26, Application US/10359460 Publication No. US20030147911A1
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LENGTH: 596
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Best Local Similarity
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APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Alderson, Mark
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; Pred. No. 1.2e-145;
0; Mismatches 0;
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APPLICANT: Dillon, Davin C.
APPLICANT: Alderson, Mark
APPLICANT: Alderson, Mark
APPLICANT: Compos-Neto, Antonio
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Fusion Protiens of Mycobacterium tuberculosis Antigens
TITLE OF INVENTION: Fusion Protiens of Mycobacterium tuberculosis Antigens
TITLE OF INVENTION: And Their Uses
FILE REFERENCE: 014058-009020US
CURRENT APPLICATION NUMBER: US/09/25,460
CURRENT FILING DATE: 2003-02-05
PRIOR APPLICATION NUMBER: US/09/287,849
PRIOR APPLICATION NUMBER: US/09/287,849
PRIOR APPLICATION NUMBER: US/09/287,849
PRIOR FILING DATE: 1997-03-13
PRIOR FILING DATE: 1997-03-13
PRIOR FILING DATE: 1997-03-13
PRIOR APPLICATION NUMBER: US 08/942,578
PRIOR APPLICATION NUMBER: US 09/025,197
PRIOR APPLICATION NUMBER: US 09/025,197
PRIOR APPLICATION NUMBER: US 09/025,56
PRIOR APPLICATION NUMBER: US 09/025,56
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-04-07
PRIOR FILING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 46
LENGTH: 596

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LAMPI COMPANIE Brannon, Mark

APPLICANT: Guderian, Jeffrey
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Heterologous Fusion Protein Constructs Comprising a
TITLE OF INVENTION: Leishmania Antigen
FILE REFERENCE: 014058-012010US
CURRENT APPLICATION NUMBER: US/10/098,732A
CURRENT FILING DATE: 2003-04-29
PRIOR APPLICATION NUMBER: US 60/275,837
PRIOR FILING DATE: 2001-03-13
NUMBER OF SEQ ID NOS: 80
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 20
LENGTH: 596
TYPE: PRT
ORGANIC"
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                                                                                                                         ; OTHER INFORMATION: Description of Artificial Sequence:bi-fusion ; OTHER INFORMATION: protein TbH9-Ra35 (designated MTB59F) US-10-098-732A-20
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Matches 391
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ORGANISM: Artificial
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Similarity 100.0%;
91; Conservative 0;
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MVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG
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; Pred. No. 1.2e-145;
0; Mismatches 0;
                                                          Score 1949; DB 12;
Pred. No. 1.2e-145;
Mismatches 0;
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                                                                                                                                                                                                                      ; LENGTH: 600
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:tri-fusion
US-09-287-849-22
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PRIOR FILING DATE: 1997-33-13
PRIOR PRIOR PILING DATE: 1997-10-01
PRIOR FILING DATE: 1997-10-01
PRIOR FILING DATE: 1997-10-01
PRIOR EPILING DATE: US 09/025,197
PRIOR PILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 09/056,556
PRIOR APPLICATION NUMBER: US 09/056,556
PRIOR FILING DATE: 1998-04-07
PRIOR FILING DATE: 1998-04-07
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SEQ ID NO 22
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APPLICANT:
APPLICANT:
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APPLICANT: Corixa Corporation
TITLE OF INVENTION: Fusion Protiens of M
TITLE OF INVENTION: and Their Uses
FILE REFERENCE: 014058-009020US
CURRENT APPLICATION NUMBER: US/09/287,849
CURRENT FILLING DATE: 1999-04-07
DEFICE APPLICATION NUMBER: US/08/818 112
                                                                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 1998-04-07
PRIOR APPLICATION NUMBER: US
PRIOR FILING DATE: 1998-12-30
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APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
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                                                                                                                                                                    Local Similarity
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SSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI
                                                                        MVDFGALPPEINSARMYAGPGSASLVAAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG
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                                                                                                                                                                  Score 1949; DB 9;
Pred. No. 1.2e-145;
                                                                                                                                                    Mismatches
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TITLE OF INVENTION: Fusion protiens of Mycobacterium tuberculosis Antigens
FILE OF INVENTION: and Their Uses
FILE REFERENCE: 014058-009020US
CURRENT APPLICATION NUMBER: US/10/359,460
CURRENT FILING DATE: 2003-02-05
PRIOR APPLICATION NUMBER: US/9/287,849
PRIOR FILING DATE: 1999-04-07
PRIOR FILING DATE: 1999-03-13
PRIOR FILING DATE: 1997-03-13
PRIOR FILING DATE: 1997-03-13
PRIOR APPLICATION NUMBER: US 08/942,578
PRIOR APPLICATION NUMBER: US 08/942,578
PRIOR APPLICATION NUMBER: US 09/025,197
PRIOR APPLICATION NUMBER: US 09/025,197
PRIOR APPLICATION NUMBER: US 09/025,56
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-04-07
PRIOR PRIOR PRIOR DATE: 1998-04-07
PRIOR PRIOR PRIOR DATE: 1998-04-07
PRIOR FILING DATE: 1998-12-30
NUMBER: US 09/223,040
PRIOR FILING DATE: 1998-12-30
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US-10-359-460-22
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Best Local Similarity
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SEQ ID NO 22
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APPLICANT:
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TYPE: PRT
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APPLICANT: Skei
APPLICANT: Dill
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                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Artificial Sequence FEATURE:
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          121
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                                                                                   SSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAAYETAYGLTVPPPVIAENRAELMI 120
        LIATNLLGQNTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATLLPFEEAPEMTSAGG 180
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                                                                                                                                 MVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG
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Skeiky, Yasir A.W.
Dillon, Davin C.
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Pred. No. 1.2e-145;
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APPLICANT: Guderian, Jeffrey
APPLICANT: Corixa Corporation
ITILE OF INVENTION: Heterologous Fusion Protein Constructs Comprising a
TITLE OF INVENTION: Heterologous Fusion Protein Constructs Comprising a
TITLE OF INVENTION: Leishmania Antigen
FILE REFERENCE: 014058-012010US
CURRENT APPLICATION NUMBER: US/10/098,732A
CURRENT APPLICATION NUMBER: US/10/098,732A
CURRENT FILING DATE: 2003-04-29
PRIOR APPLICATION NUMBER: US 60/275,837
PRIOR APPLICATION NUMBER: US 60/275,837
PRIOR ESEQ ID NOS: 80
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 18
LENGTH: 729
TYPE: PRT
ORGANISM: Artificial Sequence
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; OTHER INFORMATION: Description of Artificial
; OTHER INFORMATION: (Ral2-TbH9-Ra35MutSA)
US-10-098-732A-18
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APPLICANT: Brannon, Mar
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Pred. No. 1.6e-145;
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APPLICANT: Guderian, Jeffrey
APPLICANT: Coriva Corporation
TITLE OF INVENTION: Heterologous Fusion Prote
TITLE OF INVENTION: Leishmania Antigen
FILE REFERENCE: 014058-012010US
CURRENT APPLICATION NUMBER: US/10/098,732A
CURRENT FILING DATE: 2003-04-29
PRIOR APPLICATION NUMBER: US 60/275,837
PRIOR APPLICATION NUMBER: US 60/275,837
PRIOR FILING DATE: 2001-03-13
NUMBER OF SEQ ID NOS: 80
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 65
RESULT 11
US-09-287-849-2
; Sequence 2, Ap
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US-10-098-732A-65
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APPLICANT: Brannon,
APPLICANT: Guderiar
APPLICANT: Corixa (
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TYPE: PRT
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Patent No. US20020009459A1

Application

US/09287849

RESULT 12 US-10-359-460-2

Sequence 2, Application US/10359460 Publication No. US20030147911A1 GENERAL INFORMATION:

APPLICANT: Reed, Steven G. APPLICANT: Skeiky, Yasir A.W. APPLICANT: Dillon, Davin C.

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; TYPE: PRT; ORGANISM: Artificial Sequence; FEATURE: ; FEATURE: OTHER INFORMATION: Description of Artificial Sequence:tri-fusion US-09-287-849-2
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CURRENT APPLICATION NUMBER: US/09/287,849
CURRENT FILING DATE: 1999-04-07
PRIOR APPLICATION NUMBER: US 08/818,112
PRIOR FILING DATE: 1997-03-13
PRIOR APPLICATION NUMBER: US 08/942,578
PRIOR FILING DATE: 1997-10-01
PRIOR APPLICATION NUMBER: US 09/025,197
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-04-07
PRIOR APPLICATION NUMBER: US 09/056,556
PRIOR APPLICATION NUMBER: US 09/056,556
PRIOR APPLICATION NUMBER: US 09/223,040
PRIOR PRILING DATE: 1998-04-07
PRIOR FILING DATE: 1998-04-07
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APPLICANT: Skelky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Alderson, Mark
APPLICANT: Campos-Neto, Antonio
APPLICANT: Compos-Neto, Antonio
TITLE OF INVENTION: Fusion Protiens of
TITLE OF INVENTION: and Their Uses
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SOFTWARE: PatentIn Ve
SEQ ID NO 2
LENGTH: 729
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Best Local :
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GQMGARAGGGLSGVLRVPPRPYVMPHSPAAG 391
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Pred. No. 3.9e-145;
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TITLE OF INVENTION: Fusion protiens of Mycobacterium tuberculosis Antigens
TITLE OF INVENTION: and Their Uses
FILE REFERENCE: 014058-009020US
CURRENT APPLICATION NUMBER: US/10/359,460
CURRENT APPLICATION NUMBER: US/9/287,849
PRIOR APPLICATION NUMBER: US/9/287,849
PRIOR FILING DATE: 1999-04-07
PRIOR APPLICATION NUMBER: US 08/818,112
PRIOR APPLICATION NUMBER: US 08/942,578
PRIOR APPLICATION NUMBER: US 08/925,197
PRIOR APPLICATION NUMBER: US 09/025,197
PRIOR APPLICATION NUMBER: US 09/025,197
PRIOR APPLICATION NUMBER: US 09/025,397
PRIOR APPLICATION NUMBER: US 09/025,397
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 09/025,56
PRIOR FILING DATE: 1998-04-07
; Sequence 16, Application US/10098732A
    Publication No. US20030175294A1
    GENERAL INFORMATION:
    APPLICANT: Skeiky, Yasir
    APPLICANT: Brannon, Mark
    APPLICANT: Guderian, Jeffrey
    APPLICANT: Corixa Corporation
    TITLE OF INVENTION: Heterologous Fusion Pr
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US-10-098-732A-16
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US-10-359-460-2
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LENGTH: 729
TYPE: PRT
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Pred. No. 3.9e-145;
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Mismatches
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RESULT 14
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                                                                                                                                                                    Sequence 111, Applicate Publication No. US2003 GENERAL INFORMATION:
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PRIOR FILING DATE: 2001-03-13
NUMBER OF SEQ ID NOS: 80
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 16
LENGTH: 729
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CURRENT APPLICATION NUMBER: US/10/098,732A
CURRENT FILING DATE: 2003-04-29
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ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of
OTHER INFORMATION: protein MTB72F
OTHER INFORMATION: fusion)
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Houghton, Raymond
Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
Hendrickson, Ronald C.
Hendrickson, Ronald SAND MI
AND DIAGNOSIS OF
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                                                                                                                                                                                                        Application US/10084843
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                                                                                                          Skeiky, Yasir A.W.
Dillon, Davin C.
Campos-Neto, Antonio
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Pred. No. 3.9e-145;
0; Mismatches 1;
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NUMBER OF SEQUENCES: 355
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP

METHODS FOR IMMUNOTHERAPY
OF TUBERCULOSIS

STREET: 6300 Columbia Center,

701

Fifth Avenue

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US-10-193-002-106
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                                                                                               Sequence 106, Applicat Publication No. US2003 GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 111: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: MAKI, DAVId J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/10/084,843
FILING DATE: 25-Feb-2002
CLASSIFICATION: Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                             APPLICANT:
                                                                                                                                                                                                                                                                       357
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                                                                                                                                                                                                                                                                                                             GSSGLGAGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAQTAPGHMLG
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TELEFAX: (206) 682-6031
                                                                                                                 Application US/10193002
o. US20030135026A1
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                  Skeiky, Yasir A.W.
Dillon, Davin C.
Campos-Neto, Antonia
                                                                          Reed, Steven G.
Houghton, Raymond
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Pred. No. 1.96
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APPLICATION NUMBER: US/09/072,596

FILING DATE: 05-MAY-1998

ATTORNEY/AGENT INFORMATION:

NAME: MAKI, DAVId J.

REGISTRATION NUMBER: 31,392

REFERENCE/DOCKET NUMBER: 210121.417C9

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 622-4900

TELEPHONE: (206) 622-4900

TELEPHONE: (206) 682-6031

INFORMATION FOR SEQ ID NO: 106:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: US/10/193,002
FILING DATE: 10-Jul-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
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ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center,
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TITLE OF INVENTION: COMPOUNDS AND
TUBERCULOSIS
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                                      GLPVGQMGARAG--GGLSGVLRVPPRPYVMPHSPAAG 391
                                                                                                       GSSGLGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAERGPGQMLG
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STATE: Washington
  GLPLGQLTNSGGGFGGVSNALRMPPRAYVMPRVPAAG
                                                                             GSSGLGAGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAQTAPGHMLG
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TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
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Twardzik, Daniel
Lodes, Michael J.
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84.9%; Pred. No. 1.9e-122;
tive 19; Mismatches 34; I
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Search completed: November 21, 2003, 17:11:03  $\,$  Job time : 34  $\,$  secs

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Match
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1: /cgn2_6/ptodata/1/paa/PCT_NEW_COMB.pep:*

2: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep:*

3: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep:*

4: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:*

5: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:*

6: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:*

7: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:*
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MVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAMSSLGSSLGSSG

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LLEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN

LLEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN

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SSAGLMVAĀASPYVAWMSVTAGQAELTAĀQVRVAĀAĀYETĀYGLTVPPPVIĀENRĀELMI

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					OR APPLICATION NUMBER: US 09/597,796 OR FILING DATE: 2000-06-20 OR APPLICATION NUMBER: US 60/265,737 OR FILING DATE: 2001-02-01	0 60/3	: US 06-2 : US 02-0	2000- NUMBER 2001-	DATE:	APPLIC FILING APPLIC FILING	; PRIOR APPLICATION NUMBER: US 09/597,796 ; PRIOR FILING DATE: 2000-06-20 ; PRIOR APPLICATION NUMBER: US 60/265,737 ; PRIOR FILING DATE: 2001-02-01	
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APPLICANT: Skeiky, Yasir
APPLICANT: Reed, Steven
APPLICANT: Alderson, Mark
APPLICANT: Alderson, Mark
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tub
FILE REFERENCE: 014058-009070US
CURRENT APPLICATION NUMBER: US/09/886,349A
CURRENT FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: US 09/597,796
PRIOR APPLICATION NUMBER: US 60/265,737
PRIOR FILING DATE: 2001-02-01
NUMBER OF SEQ ID NOS: 50
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Sequence 2, Application US/10369983
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SEQ ID NO 20
LENGTH: 596
TYPE: PRT
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Pred. No. 1.3e-108;
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APPLICANT: Guderian, Jeff
APPLICANT: Reed, Steven
APPLICANT: Corixa Corporation
FILE REFERENCE: 014058-099881US
CURRENT APPLICATION NUMBER: US/10/369,983
CURRENT FILING DATE: 2003-02-18
PRIOR APPLICATION NUMBER: US 60/357,351
PRIOR APPLICATION NUMBER: US 60/357,351
PRIOR FILING DATE: 2002-02-15
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 723
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APPLICANT: Corixa Corporation
TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
FILE REFERENCE: 014058-09070US
CURRENT APPLICATION NUMBER: US/09/886,349A
CURRENT FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: US 09/597,796
PRIOR FILING DATE: 2000-06-20
PRIOR APPLICATION NUMBER: US 60/265,737
PRIOR PRIOR PRIOR APPLICATION NUMBER: US 60/265,737
PRIOR FILING DATE: 2001-02-01
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Patentin Ver. 2.1
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APPLICANT: Reed, Steven
APPLICANT: Alderson, Mark
APPLICANT: Corixa Corporat
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TYPE: PRT
ORGANISM: Artificial Sequence
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CURRENT APPLICATION NUMBER: US/10/369,983
; CURRENT FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/357,351
; PRIOR FILING DATE: 2002-02-15
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 21
; SEQ ID NO 21
; SEQ ID NO 27
; TYPE: PRI
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence:MTB72F
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OTHER INFORMATION:
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US-09-886-349A-18
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                                                                                                               US-10-369-983-21
                                                                                                                                                                                                                                                                                        Sequence 21, Application US/10369983
GENERAL INFORMATION:
APPLICANT: Skeiky, Yasir
APPLICANT: Guderian, Jeff
APPLICANT: Reed, Steven
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Fusion Proteins of Mycobacterium
FILE REFERENCE: 014058-009081US
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Matches
                                                       Matches 391;
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Best Local Similarity
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                                                      Score 1949; DB 6;
Pred. No. 1.6e-108;
0; Mismatches 0;
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Pred. No. 1.6e-108;
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RESULT 6
US-10-369-983-22
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TITLE OF INVENTION: Fusion Proteins of Mycobacterium
FILE REFERENCE: 014058-009081US
CURRENT APPLICATION NUMBER: US/10/369,983
CURRENT FILING DATE: 2003-02-18
PRIOR APPLICATION NUMBER: US 60/357,351
PRIOR FILING DATE: 2002-02-15
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 22, Application US/10369983
GENERAL INFORMATION:
APPLICANT: Skeiky, Yasir
APPLICANT: Guderian, Jeff
APPLICANT: Reed, Steven
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OTHER INFORMATION:
OTHER INFORMATION:
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TYPE: PRT
ORGANISM: Artificial Sequence
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                                                                                     LLEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN
                                                                                                                                                                              LIATNLLGQNTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATLLPFEEAPEMTSAGG
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Pred. No. 1.6e-108;
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RESULT 8
US-10-369-983-14
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US-10-369-983-15
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Best Local Similarity
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TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
FILE REFERENCE: 014058-009081US
CURRENT APPLICATION NUMBER: US/10/369,983
CURRENT FILING DATE: 2003-02-18
PRIOR APPLICATION NUMBER: US 60/357,351
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APPLICANT: Guderian, Jeff
APPLICANT: Reed, Steven
APPLICANT: Corixa Corporat
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NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn Ver. 2.1
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TYPE: PRT
ORGANISM: Artificial Sequence
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Pred. No. 1.9e-108;
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        SOFTWARE: PatentIn V
SEQ ID NO 13
LENGTH: 875
TYPE: PRT
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PRIOR FILING DATE: 2002-02-15
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 14
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Best Local Similarity
                                                                   APPLICANT: Skeiky, Yasir
APPLICANT: Guderian, Jeff
APPLICANT: Guderian, Jeff
APPLICANT: Reed, Steven
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
FILE REFERENCE: 014058-009081US
CURRENT APPLICATION NUMBER: US/10/369,983
CURRENT FILING DATE: 2003-02-18
PRIOR APPLICATION NUMBER: US 60/357,351
PRIOR APPLICATION NUMBER: US 60/357,351
PRIOR APPLICATION DATE: 2002-02-15
NUMBER OF SEQ ID NOS: 22
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ORGANISM: Artificial
FEATURE:
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APPLICANT: Skeiky, Yasir
APPLICANT: Guderian, Jeff
APPLICANT: Guderian, Jeff
APPLICANT: Reed, Steven
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
FILE REFERENCE: 014058-009081US
CURRENT APPLICATION NUMBER: US/10/369,983
CURRENT FILING DATE: 2003-02-18
CURRENT FILING DATE: 2003-02-16
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Pred. No. 1.9e-108;
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APPLICANT: Skeiky, Yasir
APPLICANT: Guderian, Jeff
APPLICANT: Guderian, Jeff
APPLICANT: Reed, Steven
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
FILE REFERENCE: 014058-009081US
CURRENT APPLICATION NUMBER: US/10/369,983
CURRENT FILING DATE: 2003-02-18
PRIOR APPLICATION NUMBER: US 60/357,351
PRIOR FILING DATE: 2002-02-15
INUMBER OF 520 ID NOS: 22
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 12
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SSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAAYETAYGLTVPPPVIAENRAELMI 120
                               MVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG
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                                                                                                                                                                                   Description of Artificial Sequence: fusion R95F (MTB72F-MAPS)
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                                                                                           100.0%; Score 1949; DB 6; 100.0%; Pred. No. 2.2e-108; ... Mismatches 0;
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100.0%; Pred. No. 2e-108;
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US-10-369-983-4
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PRIOR FILING DATE: 2002-02-15
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
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APPLICANT: Guderian, Jeff
APPLICANT: Reed, Steven
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
FILE REFERENCE: 014058-009081US
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                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Description OTHER INFORMATION: protein
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Pred. No. 2.4e-108;
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PRIOR APPLICATION NUMBER: US 60/357,351
PRIOR FILING DATE: 2002-02-15
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 18
LENGTH: 1016
TYPE: PRT
ORGANISM: Artificial Sequence
                                 WS-10-369-983-17
Sequence 17, Application US/10369983; GENERAL INFORMATION:
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GENERAL INFORMATION:
APPLICANT: Skeiky, Yasir
APPLICANT: Guderian, Jeff
APPLICANT: Reed, Steven
APPLICANT: Corixa Corporation
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APPLICANT: Skeiky, Yasir APPLICANT: Guderian, Je
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CURRENT FILING DATE: 2003-02-18
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TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
FILE REFERENCE: 014058-009081US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Description of Artificial Sequence:fusion OTHER INFORMATION: MTB103F (MTB72F-85b)
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 Guderian, Jeff
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Pred. No. 2.4e-108;
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SOFTWARE: PatentIn Ver. 2
SEQ ID NO 17
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Best Local
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APPLICANT: Corixa Corporation
TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
FILE REFERENCE: 014058-009081US
CURRENT APPLICATION NUMBER: US/10/369,983
CURRENT FILING DATE: 2003-02-18
PRIOR APPLICATION NUMBER: US 60/357,351
PRIOR FILING DATE: 2002-02-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Description OTHER INFORMATION: MTB102tm2F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
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                     GQMGARAGGGLSGVLRVPPRPYVMPHSPAAG
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GOMGARAGGGLSGVLRVPPRPYVMPHSPAAG
                                                                  LGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAERGPGQMLGGLPV
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Pred. No. 2.4
0; Mismatches
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RESULT 14
US-10-369-983-16
Sequence 16. Application US/10369983
GENERAL INFORMATION:
APPLICANT: Skeiky, Yasir
APPLICANT: Skeiky, Yasir
APPLICANT: Guderian, Jeff
APPLICANT: Corixa Corporation
TITLS OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
FILE REFERENCE: 014058-009081US
CURRENT APPLICATION NUMBER: US/10/369,983
CURRENT FILING DATE: 2003-02-18
PRIOR APPLICATION NUMBER: US 60/357,351
PRIOR PRIOR APPLICATION NUMBER: US 60/357,351
PRIOR PRIOR APPLICATION NUMBER: US 60/357,351
PRIOR APPLICATION NUMBER: US 60/357,351
PRIOR APPLICATION VET. 2.1
SOFTWARE: Patentin Ver. 2.1
SOFTWARE: Patentin Ver. 2.1
CURGIN: 1154
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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Sequence 16, Application US/09886349A

GENERAL INFORMATION:
APPLICANT: Skelky, Yasir
APPLICANT: Reed, Steven
APPLICANT: Alderson, Mark
APPLICANT: Alderson, Mark
APPLICANT: Corixá Corporation
FILLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
FILE REPERENCE: 014058-009070US
CURRENT APPLICATION NUMBER: US/09/886,349A
CURRENT FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: US 60/265,737
PRIOR APPLICATION NUMBER: US 60/265,737
PRIOR APPLICATION NUMBER: US 60/265,737
NUMBER: OF SEQ ID NOS: 50
SOFTWARE: Patentin Ver: 2.1
LENGTH: 729
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US-09-886-349A-16
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                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:tri-fusion
OTHER INFORMATION: protein MTB72F (Ral2-TbH9-Ra35 or MTB32-MTB39
OTHER INFORMATION: fusion)
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MVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG
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                                                                     Score 1944; DB 5;
Pred. No. 3.3e-108;
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Search completed: November 21, 2003, 17:10:17
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Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	% Query Match	% Query Match Length DB	BG	ID	Description
ב ב	1949	100.0	391	18	AAW32449	Mycobacterium tube
2	1949	100.0	391	18	AAW32381	Mycobacterium tube
ω	1949	100.0	391	19	AAW81702	M. tuberculosis im
4	1949	100.0	391	19	AAW64335	Mycobacterium tube
ហ	1949	100.0	391	20	AAY39132	. M. tuberculosis an
6	1949	100.0	391	20	AAY38989	M. tuberculosis re
7	1949	100.0	391	20	AAY04778	Mycobacterium spec
8	1949	100.0	391	22	AAU01888	M. tuberculosis an
9	1949	100.0	391	23	AAE29707	Mycobacterium sp.

4 4 4 5 4 3	41 42	4 9 0	38	37	ب س ب	34	သ	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10
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Mycobacterium tube Mycobacterium tube M. tuberculosis an		Antigenic fusion p Mycobacterium tube			M. tuberculosis an	cobacterium tu	M. tuberculosis im	tuberculosis	M. tuberculosis an	cobacterium tu	ılosis i	μ.		Mycobacterium spec		Mycobacterium spec	M. tuberculosis an	Mycobacterium sp.	M. tuberculosis an	M. tuberculosis an	Mycobacterium spec	Mycobacterium sp.	Ral2-H9-32A fusion	Antigenic fusion p	rium tub		Mycobacterium spec	Mycobacterium sp.	tub	

## ALIGNMENTS

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RESULT 1
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AC AAW3
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01-SEP-1995;
22-SEP-1995;
22-MAR-1996;
05-JUN-1996;
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                                   Campos-neto A, Dillon DC,
Twardzik DR, Vedvick TH;
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95US-0523436.
95US-0533634.
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1997-192903/17

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                                                                                                                                        Mycobacterium
                                                                                                                                                                                         Antigen; immunogen; vaccine; skin testing; M.tuberculosis
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useful in vaccines
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ion or treatment of tuberculosis, a
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01-SEP-1995;
22-SEP-1995;
22-MAR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A new immunogenic polypeptide has been developed comprising an immunogenic part of a soluble Mycobacterium tuberculosis antigen (or its variant differing only in conservative substitutions and/or modifications). The present sequence represents a M. tuberculosis antigen, TbH-9FL The immunogenic polypeptide can be used to diagnose M.tuberculosis infection by forming complexes with specific antibodies in the sample. Fragments of pulyaes with specific polypeptide can be used as diagnostic primers or probes and agents that bind to the antigen, especially monoclonal antibodies or equivalent polyclonal antibodies, are also used for diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New immunogenic polypeptide(s) from soluble M. tuberculosis antigens - useful for diagnosis of M. tuberculosis infection
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N-PSDB; AAT91455.
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Twardzik DR, Vedvick
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                                                                                                                                                                                                                                                                                                                                                                                              391;
                                                                                                                                                                                                                                                                                                                                                          1 MVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG
                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                  MVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAMSSLGSSSLGSSG
                                                                                                                                                                                                                                            LIATNLLGONTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATATLLPFEEAPEMTSAGG
                 GQMGARAGGGLSGVLRVPPRPYVMPHSPAAG
                                                                      LGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAERGPGQMLGGLPV
                                                                                                               MVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAMSSLGSSLGSSG
                                                                                                                                                                                      LLEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN
                                                                                                                                                                                                                            LIATNLLGQNTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATLLPFEEAPEMTSAGG
                                                                                                                                                                                                                                                                                SSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI
                                                                                                                                                                                                                                                                                                    SSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI
                                                                                                                                                                                                                                                                                                                                       MVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG
GQMGARAGGGLSGVLRVPPRPYVMPHSPAAG
                                                                                                                                                                     LLEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN
                                                                                                                                                                                                                                                                                                                                                                                                                                                  391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Page 150-152; 190pp;
                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dillon DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96US-0680573.
95US-0523435.
95US-0532136.
96US-0620280.
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                                                                                                                                                                                                                                                                                                                                                                                                        100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DC,
                                                                                                                                                                                                                                                                                                                                                                                             <u>,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Houghton
                                                                                                                                                                                                                                                                                                                                                                                           Score 1949; DB 18;
Pred. No. 4.8e-143;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Reed
 391
                            391
                                                                                                                                                                                                                                                                                                                                                                                                                       DB 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SG,
                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                       Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Skeiky YAW;
                                                                                                                                                                                                                                                                                                                                                                                                                       391;
                                                                                                                                                                                                                                                                                                                                                                                             0;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            for inducing protective immunity against tuberculosis (TB). This sequence can be formulated into vaccines and/or pharmaceutical compositions for immunising against M. tuberculosis infection or may be used for the diagnosis of tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence represents an immunogenic portion of a soluble Mycobacterium tuberculosis (MT) antigen which can be used in a method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 3B; Page 128-129; 230pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Immunogenic Mycobacterium tuberculosis polypeptide(s) and DNA - us
to develop products for the detection of M. tuberculosis infection
and for diagnosis, treatment and prevention of tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     M. tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAV64503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1998-261042/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Campos-Neto A, Dillon DC, Houghton R, Lo
Reed SG, Skeiky YAW, Twardzik DR, Vedvick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-MAR-1997;
11-OCT-1996;
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361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    osis; immunogenic; soluble; antigen; protective pharmaceutical; infection; diagnosis.
                                                                                                                                                                                                                                                                        LLEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN
                                                                                                                                                                                                                                                                                                                                                          LIATNLLGQNTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATLLPFEEAPEMTSAGG
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                          GQMGARAGGGLSGVLRVPPRPYVMPHSPAAG 391
                                                                                                     LGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAERGPGQMLGGLPV
                                                                                                                                                                                            MVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAMSSLGSSLGSSG
                                                                                                                                                                                                                                                                                                                                LIATNLLGQNTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATLLPFEEAPEMTSAGG
                                                                                                                                                                                                                                                                                                                                                                                                                SSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI
                                                                                                                                                                                                                                                                                                                                                                                                                                             SSAGLMVAAAS PYVAWMS VTAGQAEL TAAQVR VAAAA YETAYGLTVPPPVI AENRAELMI
GOMGARAGGGLSGVLRVPPRPYVMPHSPAAG
                                                                                                                                                              MVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAMSSLGSSLGSSG
                                                                                                                                                                                                                                              LLEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     391 AA;
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96US-0730510
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 1949; DB 19; 100.0%; Pred. No. 4.8e-143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                /PQAWAAANQAVTPAARALPLTSLTSAAERGPGQMLGGLPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lodes MJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This polypeptide comprises Mycobacterium tuberculosis antigen
ThH-9FL. It is encoded by genomic DNA (see AAV4435) isolated from a
M. tuberculosis strain H37RV genomic library using a probe from
C clone TbH-9 (see AAV44371). The invention relates to compositions
and methods for diagnosing tuberculosis. It provides polypeptides
(see AAW64291-W64379) comprising an antigenic portion of a soluble
M. tuberculosis antigen, as well as DNA sequences encoding such
tuberculosis antigen, as well as DNA sequences encoding such
polypeptides, recombinant expression vectors and transformed or
transfected host cells. Also claimed are methods and diagnostic
kits for detecting M. tuberculosis infection in a patient using
these polypeptides, antibodies or oligonucleotide probes and
c primers, for the diagnosis of tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 391; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated Mycobacterium tuberculosis polypeptides and DNA - use to develop products for the detection of M. tuberculosis infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1998-251292/22
N-PSDB; AAV44395.
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Reed SG, Skeiky
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-MAR-1997;
11-OCT-1996;
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LLEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN
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                                                                                                              LIATNLLGQNTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATATATLLPFEEAPEMTSAGG
                                                                                                                                                                                                                       SSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI
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                                                                                                                                                                                          SSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI
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cy YAW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97US-0818111.
96US-0729622.
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Twardzik DR, Vedvick TS;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 1949; DB 19;
Pred. No. 4.8e-143;
                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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                                                                                                         Query Match
Best Local S
Matches 391
                                                                                                                                                                                                                                                          The present invention describes polypeptides comprising an immunogenic part of a Mycobacterium tuberculosis antigen (Ag). Also described are vaccines and fusion protein containing M. tuberculosis Ag's.

M. tuberculosis Ag's, DNAs encoding them, derived fusion proteins and other polypeptides fragments, can be used in pharmaceutical compositions or vaccines to generate a protective or therapeutic immune response to M. tuberculosis and as reagents in skin tests for diagnosis of tuberculosis Ag can induce proliferation of, or cytokine secretion by, T, B or natural killer cells and/or macrophages in by, T, B or natural killer cells and/or macrophages in the secretion by, T, B or natural killer cells and/or macrophages in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1999-527409/44.
N-PSDB; AAZ19305.
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18-FEB-1998;
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                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New antigens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Campos-Neto
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mycobacterium tuberculosis; M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-NOV-1999
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                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORIXA
                                 MVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ns from Mycobacterium tuberculosis useful in diagnostic and protective or therapeutic vaccines or compositions
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                                                                                                         Conservative
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SG, Skeiky
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YAW, Twardzik DR,
                                                                                                    Score 1949; DB 20;
Pred. No. 4.8e-143;
; Mismatches 0;
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nisation; vaccine; infection;
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                                                                                                                                                                                                                                                                                                                                                                                                           Antigen; vaccine;
                      This invention describes novel recombinant antigens and their encoding nucleic acids derived from Mycobacterium tuberculosis. The novel polypeptides are useful for detecting M. tuberculosis infection in a biological sample by detecting antibodies which bind with the polypeptides, and are useful as vaccines for immunizing against M. tuberculosis infection. The new detection methods are needed as current vaccination strategies do not provide 100% immunity.
                                                                                                                                                                                                            Campos-Neto A,
Lodes MJ, Reed
Sequence
                                                                                                                                                New polypeptide comprising antigenic portions
                                                                                                                                                                                     WPI; 1999-527416/44.
                                                                                                                                                                                                                                                                        05-MAY-1998;
18-FEB-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                       diagnosis;
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SG, Skeiky
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YAW, Twardzik DR,
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R, Vedvick
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                                                                                                                                                                                                                     Gicquel B, Guigueno A;
Sequences AAY04742-Y05000 and AAY07201-Y07204 represent secreted proteins from various Mycobacterium species microorganisms. The encoding nucleotide sequences can be used as primers and probes
                                                                                             Mycobacterial DNA vectors containing reporter constructs identifying coding or promoter sequences involved in infection-associated protein expression
                                                                                                                                                                      WPI; 1999-181045/15.
N-PSDB; AAX34030.
                                                                                                                                                                                                                                                                                                     11-SEP-1997;
14-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Secreted protein; Mycobacterium; primer; PCR; hybridisation; detection; vaccine; immunisation
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methods for detecting and identifying mycobacteria, especially belonging to the M. tuberculosis complex. The encoded proteins can be used in vaccines for immunisation against a bacterial or viral infection.
                                                         WPI; 2001-290576/30.
N-PSDB; AAS03779.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  M. tuberculosis
Vaccinating against Mycobacteria infections in mammals using proteins comprising combinations of heterologous antigens
                                                                                                                                                                                              07-OCT-1999;
07-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                   Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                    TbH9; Mtb39A; antigen; vaccine; tuberculosis; acquired immunodeficiency disease.
                                                                                                                                                                                                                                                  10-OCT-2000; 2000WO-US28095
                                                                                                                                                                                                                                                                                         12-APR-2001.
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Pred. No. 4.8e-143;
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Best Local (
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                Skeiky
                                                                                                                                                                                                                 Vaccine; immunity;
                                                                                                                                                                                                                                                                           27-JAN-2003
                                                                                                                                                                                                                                                                                                                                  AAE29707 standard; Protein;
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                                                                      13-MAR-2001; 2001US-275837P
                                                                                                 13-MAR-2002; 2002WO-US08223
                                                                                                                              19-SEP-2002.
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                                                                                                                                                                                                                                           Mycobacterium sp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LLEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LIATNILIGONTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATLILPFEEAPEMTSAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SSAGLMVAAAS PYVAWMS VTAGQAELTAAQVRVAAAA YETA YGLTVPPPVI AENRAELMI
                                                                                                                                                                                                                                                                                                                                                                                                        GQMGARAGGGLSGVLRVPPRPYVMPHSPAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                               LGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAERGPGQMLGGLPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG
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                Brannon
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                                                                                                                                                                                                                                           TbH9FL antigenic protein
              Z,
                                                                                                                                                                                                                 diagnostic agent; gene therapy; TbH9FL antigen.
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                Guderian
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Pred. No. 4.8e-143;
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Matches

391;

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Query Match
                                                                                                                                              fusion polypeptide. The recombinant nucleic acid comprises a heterologous polynucleotide sequence encoding an antigen or an antigenic fragment from Mycobacterium sp. and a Leishmania polynucleotide sequence encoding a polypeptide or its fragment. The Leishmania polynucleotide is selected from TSA, Leif, M15, and 6H polynucleotides. Sequences of the invention are used in methods for eliciting immune response in mammals. They are useful as vaccines to eliciting immune response in membals. They are nicroorganisms such as Leishmania and Mycobacterium tuberculosis. Fusion polypeptides are used for enhancing the expression of polynucleotides, as in vivo diagnostic agents and for raising antibodies in a non-human animal. The invention is used in gene therapy. The present sequence is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New recombinant nucleic acid molecule comprising a Leishmania TSA, LeIF, M15 or 6H polynucleotide, useful as vaccine to elicit protec immunity against pathogenic microorganisms e.g. Leishmania and Mycobacterium tuberculosis
                                                                                                                                  Mycobacterium sp. TbH9FL antigenic protein.
                                                                                                                                                                                                                                                                                                                                                                                                               The invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 86-87; 155pp; English
                            Local
                            Similarity
                                                                                             391
100.0%; ilarity 100.0%; Conservative 0
                                                                                                                                                                                                                                                                                                                                                              relates to a recombinant nucleic acid molecule encoding a ptide. The recombinant nucleic acid comprises a heterologous
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Score 1949; DB 23;
Pred. No. 4.8e-143;
Mismatches 0;
                                              Length
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                                                                                                                                      MVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAMSSLGSSLGSSG
                                                                                                                                                                                              LLEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN
                                                                                                                                                                                                                                                                                                                 SSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI
               GQMGARAGGGLSGVLRVPPRPYVMPHSPAAG 391
                                                       LGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAERGPGQMLGGLPV
                                                                                                                                                                                                                                       LIATNLLGQNTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATALLPFEEAPEMTSAGG
                                                                                                                                                                                                                                                                                                  SSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI
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                                                                                    LGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAERGPGQMLGGLPV
                                                                                                                     MVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAMSSLGSSLGSSG
                                                                                                                                                                              LLEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN
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Mycobacterium
               Fusion protein; antigen; tuberculosis; infection;
                                          Mycobacterium
                                                            22-APR-2002
                                                                                              AAE17571
                                                                                               standard; Protein; 391
                                                           (first entry)
                                          species MTB39
                serological sensitivity;
vaccine; MTB39; TbH9 prot
                                          (TbH9) protein
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                          immune
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CC The present invention relates to fusion proteins containing at least CC two Mycobacterium species antigens, nucleotides encoding them and CC compositions comprising such fusion proteins. The present invention CC particularly relates to nucleic acids encoding fusion proteins that CC include two or more individual M. tuberculosis antigens which increase CC the serological sensitivity of sera from individuals infected with CC tuberculosis and methods for their use in diagnosis, prevention and CC treatment of tuberculosis infecteion. Sequences of the invention are CC useful for eliciting an immune response in a mammal, e.g., human, CC immunised with BCG. They are useful in the diagnosis, treatment and CC polynucleotides are useful as diagnostic tools in patients infected CC with Mycobacterium, in vitro and in vivo assays for detecting humoral CC animals or cell-mediated immunity against M. tuberculosis, for the CC diagnosis of an infection or monitoring of disease progression, as CC immunogens to generate or elicit a protective immune response in a non-human CC animal. Sequences of the invention are useful as in vivo diagnostic agents CC fusion proteins of the invention are useful as in vivo diagnostic agents CC for intradermal skin test. The present sequence is Mycobacterium species
                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 391; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-JUN-2000; 2000US-0597796.
01-FEB-2001; 2001US-265737P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Composition comprising MTB39 antigen and MTB32A antigen Mycobacterium species, useful for eliciting immune respo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Skeiky Y, Reed S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 83; Page 102-103; 136pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TbH9) protein.
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                                                                                                                                                                                                                                                                                                         SSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI 120
                                                                                  MVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAMSSLGSSLGSSG
                                                                                                                                                                     LLEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN 240
                                                                                                                                                                                                            LIATNLLGQNTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATLLPFEEAPEMTSAGG
                                                                                                                                                                                                                                                LIATNILIGONTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATATLIPFEEAPEMTSAGG
                                                                                                                                                                                                                                                                                   SSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI
                                                                                                                                                                                                                                                                                                                                                            MVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG
LGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAERGPGQMLGGLPV
                                                       MVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAMSSLGSSLGSSG
                                                                                                                                  LLEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  391 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 1949; DB 23; 100.0%; Pred. No. 4.8e-143;
                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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RESULT 11
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                                                                                   Query Match
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Matches 391
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N-PSDB;
                                                                                                                                                                                                                                                                        This sequence represents a recombinant Mycobacterium tuberculosis bi-antigen fusion protein, termed Mtb59f, composed of the antigens TbH9 and Ra35. The fusion protein is expressed in host cells using a vector carrying a polynucleotide (see AAZ20205) comprising the coding sequences for the 2 antigens. The invention provides fusion proteins (see AAY32059-71) containing at least 2 M. tuberculosis antigens. The new fusion proteins and polynucleotides encoding them are useful as vaccines for preventing tuberculosis (claimed), for diagnosis (via in vitro assays or intradermal skin tests for detection of anti-M. tuberculosis antibodies), monitoring of disease progression, and treatment of tuberculosis. They are more effective immunogens than mixtures of the individual protein
                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New fusion proteins useful for diagnosis, prevention and treatment of tuberculosis -  \\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Skeiky YAW, Alderson M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-APR-1998;
30-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY32070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Fig 12A-B; 83pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mycobacterium tuberculosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-JAN-2000
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DB; AAZZ0205.
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                                                                                                                Similarity
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MVDFGALPPBINSARMYAGPGSASLVAAAQMMDSVASDLFSAASAFQSVVMGLTVGSWIG 60
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                                                                                                                                                                                                596
                                                                                   100.0%; llarity 100.0%; Conservative 0
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erapy; vaccine; immunogen.
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98US-0223040
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                                                                                      Score 1949; DB 20;
Pred. No. 8.1e-143;
; Mismatches 0;
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RESULT 12
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AC AAE29710
AC AAE29
AC AAE29
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AC AAE20
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AAE29
AC AAE20
AAE29
AC AAE20
AAEA0
AA
                                                       The invention relates to a recombinant nucleic acid molecule encoding a fusion polypeptide. The recombinant nucleic acid comprises a heterologous polynucleotide sequence encoding an antigen or an antigenic fragment from Mycobacterium sp. and a Leishmania polynucleotide sequence encoding a polypeptide or its fragment. The Leishmania polynucleotide is selected from TSA, LeFF, M15, and 6H polynucleotides. Sequences of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Skeiky
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vaccine; immunity; diagnostic Ra35; MTB59F; fusion protein.
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                                                                                                                                                                                                                                                                       Disclosure; Page
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                                                                                                                                                                                                                                                                                                                                                         recombinant nucleic acid molecule comprising a Leishmania TSA, F, M15 or 6H polynucleotide, useful as vaccine to elicit protecunity against pathogenic microorganisms e.g. Leishmania and
                                    used
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                                 for eliciting immune response in mammals. They
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tuberculosis;
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infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         species MTB59F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              serological sensitivity; immune response; vaccine; MTB59F; TbH9-Ra35 protein.
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Pred. No. 8.1e-143;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to fusion proteins containing at least two Mycobacterium species antigens, nucleotides encoding them and compositions comprising such fusion proteins. The present invention particularly relates to nucleic acids encoding fusion proteins that composition is related to nucleic acids encoding fusion proteins that compared two or more individual M. tuberculosis antigens which increase the serological sensitivity of sera from individuals infected with cuberculosis and methods for their use in diagnosis, prevention and treatment of tuberculosis infection. Sequences of the invention and cuseful for eliciting an immune response in a mammal, e.g., human, communised with BCG. They are useful in the diagnosis, treatment and prevention of Mycobacterium infection. The fusion proteins and the colynucleotides are useful as diagnostic tools in patients infected with Mycobacterium, in vitro and in vivo assays for detecting humoral custom to generate or elicit a protective immune response in a communogens to generate or elicit a protective immune response in a communal. Sequences of the invention are also used as vaccines. MTB32A custom proteins of the invention are useful as in vivo diagnostic agents continual skin test. The present sequence is Mycobacterium species of the invention are useful as in vivo diagnostic agents continuated the proteins of the invention are also used as vaccines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches 391
                                                        08-MAY-2002
                                                                                                                               AAU74599
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                 Antigenic
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                                                                                                                                                                                                                        GOMGARAGGGLSGVLRVPPRPYVMPHSPAAG
                                                                                                                                                                                                                                                                                                LGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAERGPGQMLGGLPV
                                                                                                                                                                                                                                                                                                                         LGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAERGPGQMLGGLPV
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               fusion protein Tb59-Ra35
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                                                      (first entry)
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                                                                                                                           Protein;
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Pred. No. 8.1e-143;
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                   (Mtb59f).
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                                                                                                                                                                                                                                                                                                           The invention relates to a purified polypeptide which induces an immune response of Mycobacterium tuberculosis. Polypeptides of the invention are useful for diagnosing, treating or preventing M. tuberculosis infection, particularly tuberculosis infection. In particular, the polypeptides are useful as a vaccine formulation with an adjuvant to afford long-term protection in animals against the development of tuberculosis. The protein coding sequence may be used to encode a protein product for use as an immunogen to induce and/or enhance an immune response to M. tuberculosis. This sequence represents an M. tuberculosis fusion protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Reed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New fusion proteins of Mycobacterium tuberculosis antigens, useful for diagnosing, treating or preventing M. tuberculosis infection, particularly as vaccine for treating or preventing tuberculosis >
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fusion protein; tuberculosis; Mycobacterium tuberculosis; tuberculostatic; immunogen; vaccine; Tb59-Ra35; Mtb59f.
                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Fig 12; 62pp;
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07-APR-1998;
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SKEIKY Y A.
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CAMPOS-NETO
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  LLEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN
                   LLEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN
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ilarity 100.0%;
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                                                                                                                                                                             Query Match
Best Local Sim:
Matches 391;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New fusion proteins useful for diagnosis, prevention and treatment of tuberculosis -
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30-DEC-1998;
                                                                                                                                                                                                                                                                                                      Sequence
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                                                          MVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG
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                    GQMGARAGGGLSGVLRVPPRPYVMPHSPAAG 391
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GOMGARAGGGLSGVLRVPPRPYVMPHSPAAG
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Search completed: November 21, 2003, 17:04:07 Job time : 46 secs

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Result
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Maximum Match 100%
Listing first 45 summaries
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US-08-818-111-102

US-09-056-556-102

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US-08-818-111-101

US-08-818-111-101

US-08-818-111-104

US-09-072-596-101

US-08-818-111-104

US-08-818-111-104

US-08-818-111-104

US-08-818-111-91

US-09-072-596-109

US-09-073-009-126

US-09-073-009-126

US-09-073-009-126

US-08-311-731A-208

US-08-311-731A-208

US-08-818-112-114

US-09-072-596-109
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Sequence 107, App
Sequence 102, App
Sequence 102, App
Sequence 104, App
Sequence 116, App
Sequence 116, App
Sequence 111, App
Sequence 109, App
Sequence 109, App
Sequence 104, App
Sequence 104, App
Sequence 91, Appl
Sequence 92, Appl
Sequence 92, Appl
Sequence 126, App
Sequence 127, Appl
Sequence 131, App
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126	128	129.5	129.5	129.5	131.5	139.5	141	143.5	145	186.5	186.5	215	261	261	261	261	261
6.5	6.6	6.6	6.6	6.6	6.7	7.2	7.2	7.4	7.4	9.6	9.6	11.0	13.4	13.4	13.4	13.4	13.4
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US-08-911-364-1	US-09-340-736E-1	US-09-323-433A-8	US-08-396-001-8	US-08-861-464-8	US-09-894-998A-47	US-08-678-039A-40	US-08-864-038A-3	US-09-477-135A-128	US-09-252-991A-20437	US-09-072-596-199	US-09-056-556-204	US-09-073-009-14	PCT-US94-08267-2	US-09-342-563-2	US-08-471-869-2	US-08-444-623-2	US-08-095-734-2
Sequence 1, Appli	Sequence 1, Appli	Sequence 8, Appli	Sequence 8, Appli	Sequence 8, Appli	Sequence 47, Appl	Sequence 40, Appl	Sequence 3, Appli	Sequence 128, App	Sequence 20437, A	Sequence 199, App	Sequence 204, App	Sequence 14, Appl	Sequence 2, Appli	•	•	•	Sequence 2, Appli

## ALIGNMENTS

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RESULT 1
US-08-818-112-107
; Sequence 107, Application US/08818112
; Patent No. 6280969
; GENERAL INFORMATION:
Reed, Steven G.
                                                                             US-08-818-112-107
                                                                                             INFORMATION FOR SEQ ID NO: 10
SEQUENCE CHARACTERISTICS:
LENGTH: 391 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/818,112
FILING DATE: 13-MAR-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.411C6
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-4900
                                    Query Match
    Matches
                    Best Local Similarity
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICANT: Vedvick, Thomas S.
APPLICANT: Twardzik, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
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ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
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    Conservative
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                    100.0%; Score 1949; DB 3; 100.0%; Pred. No. 2.7e-154;
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                                                                               TELEFAX: (206) 682-6031 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/818,111 FILING DATE: 13-MAR-1997 CLASSIFICATION: 424
                                                                                                                                                                                                                                                                     ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                          REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622,4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Reed, Steven G. APPLICANT: Skeiky, Yasir A
                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
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                         STRANDEDNESS:
                                                                                                                                                                      NAME: Maki,
               TOPOLOGY:
                                                    LENGTH:
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Dillon, Davin C.
Campos-Neto, Antonia
                                                    391 amino acids
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Vedvick, Thomas S.
Twardzik, Daniel R.
TWARTAIN: COMPOUNDS AND METHODS
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             linear
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US-09-056-556-107
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Sequence 107, Application US/09056556 Patent No. 6350456
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Best Local Similarity 100.
Matches 391; Conservative
                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIAN Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/09/056,556
ETLING DATE: 07-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS A
NUMBER OF SEQUENCES: 241
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                             TELEPHONE: (206) 622-49
TELEPAX: (206) 682-6031
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: (206) 622-4900
                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 6300 (
CITY: Seattle
STATE: Washing
STRANDEDNESS:
TOPOLOGY: lir
                                  LENGTH: 391 amino acids
                                                                                                                                                                                   REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
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RESULT 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patent No. 6458366
GENERAL INFORMATION:
APPLICANT: Reed,
                                                                                                                                          STREET: 6300 Columbia Center, 701 Fifth Ave CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Skeiky, Yasir A.W. APPLICANT: Dillon, Davin C.
ATTORNEY/AGENT INFORMATION:
NAME: MAKI, DAVId J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.417C9
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
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                                                                                        APPLICATION NUMBER: US/09/072,596 FILING DATE: 05-MAY-1998 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: SEED and BERRY LLP
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Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
Hendrickson, Ronald C.
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                                                                                                                                 US-09-223-040-2
                                                                                                                                                                          ; SOFTWARE: PatentIn Ver. 2
SEQ ID NO 2
; LENGTH; 729
; TYPE: PRT
; ORGANISM: Artificial Sequ
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APPLICANT: Alderson, Mark
APPLICANT: Campos-Neto, Antonio
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Fusion Proteins of
TITLE OF INVENTION: and Their Uses
FILE REFERENCE: 014058-09010US
                                                              Query Match
Best Local S
Matches 390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/09223040 Patent No. 6544522
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Best Local S
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CURRENT FILING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 10
COPTMEND DESCRIPTION OF SEQ ID NOS: 10
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                                                                                                                                             OTHER INFORMATION: Description of Artificial Sequence:tri-fusion
                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 391 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
142 MVDFGALPPEINSARMYAGPGSÄSLVÄÄÄQMWDSVÄSDLFSÄÄSAFQSVVWGLTVGSWIG
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pred. No. 1.7e-153;
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US-08-818-112-111; Sequence 111, A
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Query Match
                                                                                                               TELEFAX: (206) 682-6031 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                              APPLICATION NUMBER: US/08
PILING DATE: 13-MAR-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                               ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Houghton, Raymond
APPLICANT: Vedvick, Thomas S.
APPLICANT: Twardzik, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Reed, Steven APPLICANT: Skeiky, Yasiı
                                                                                                                                                               REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
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CITY: Seattle
STATE: Washing
                                                               STRANDEDNESS
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Dillon, Davin C.
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Score 1652.5;
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APPLICATION NUMBER: US/08/818,111
FILING DATE: 13-MAR-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.417C6
REGISTRATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 106:
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Patent No.
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Houghton, Raymond
APPLICANT: Vedvick, Thomas S.
APPLICANT: Twardzik, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
NUMBER OF SEQUENCES: 148
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIOM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
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LENGTH:
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Dillon, Davin C.
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tive 19; Mismatches 34;
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RESULT 8
US-09-056-556-111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
TELEFAX: (206) 682-603
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                             COUNTRY: USA
ZIP: 98104-7092
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, VG
CURRENT APPLICATION NUMBER: US/09/056,556
FILING DATE: 07-APR-1998
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                             ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 2101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPAX: (206) 682-6031
                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS
                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                  STREET: 6300 C
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TOPOLOGY: 1i
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                                                                                                                                                                                                                                                                                                                                 Washington
                                                                                                                                                                                                                                                                                                                                                                  6300 Columbia Center,
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Pred. No. 1.3e-
19; Mismatches
                                                                                  210121.457
                                                                                                                                                                                                                                                                                                                                                                  701 Fifth Avenue
                                                                                                                                                                                                                  Version
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L.3e-129;
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US-09-072-596-106
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Best Local Simi
Matches 337;
                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Reed, S:
APPLICANT: Skeiky,
APPLICANT: Dillon,
                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
APPLICANT:
APPLICANT:
                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
 ATTORNEY/AGENT INFORMATION: NAME: Maki, David J.
                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                            APPLICANT: Lodes, Michael J.
APPLICANT: Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                               STREET: 6300 Co
CITY: Seattle
STATE: Washing
                               APPLICATION NUMBER: FILING DATE: 05-MAN CLASSIFICATION:
                                                                                                                                 COMPUTER:
                                                                                                                                                                                 ZIP: 98104-7092
                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                             ADDRESSEE:
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TOPOLOGY: li
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Vedvick, Thomas S.
Twardzik, Daniel R.
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Dillon, Davin C.
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Pred. No. 1.3e-129;
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TUBERCULOSIS

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Patent No. 629
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 396 amino acids
              ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                   APPLICANT: Houghton, Raymond
APPLICANT: Vedvick, Thomas S.
APPLICANT: Twardzik, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
NUMBER OF SEQUENCES: 153
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
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CURRENT APPLICATION DATA:
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                                                                                                                                  STREET: 5500 STREET: Seattle
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                                                                                                                  COUNTRY:
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                                                                                                                                                                  6300 Columbia Center,
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Dillon, Davin C.
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Pred. No. 1.3e-1
9; Mismatches
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RESULT 11
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NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.411C6
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
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TYPE: amino acid
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GENERAL INFORMATION:
APPLICANT: Reed, S
APPLICANT: Skeiky,
APPLICANT: Dillon,
                                                                                                                                                                                                                                                                                                                                                               Sequence 104, Application US/08818111 Patent No. 6338852
                                                                                                                                                                                                                                              APPLICANT:
APPLICANT:
APPLICANT:
               ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                               APPLICANT: Twardzik, Daniel R. TITLE OF INVENTION: COMPOUNDS AND
                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                             COUNTRY:
                                                                                                                                 CITY: Seattle
 SOFTWARE:
                                                                                                                                                                ADDRESSEE:
                                                                                                              Washington
                                                                                                                                             E: SEED and BERRY LLP 6300 Columbia Center,
                                                                                                 USA
                                                                                                                                                                                                                                              Houghton, Raymond
Vedvick, Thomas S.
                                                                                                                                                                                                                                                                             Campos-Neto, Antonia
                                                                                                                                                                                                                                                                                              Skeiky, Yasir A.W.
Dillon, Davin C.
 PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                Steven
                                                                                                                                                                                                148
                                                                                                                                                701
                                                                                                                                                                                                                 METHODS FOR DIAGNOSIS
Version
                                                                                                                                                Fifth Avenue
 #1.30
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RESULT 12
US-09-056-556-109
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Patent No. 6350456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS
NUMBER OF SEQUENCES: 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (206) 682-6031 INFORMATION FOR SEQ ID NO:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,556
FILING DATE: 07-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 y Match 76.3%;
Local Similarity 84.2%;
nes 303; Conservative 1
                                                                                                                                                                             CITY: Seattle
STATE: Washing
                                                                                                                                           ZIP: 98104-7092
                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE: 13-MAI
                                                                                                                                                                                                                              ADDRESSEE:
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                                                                                                                                                                          Washington
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                                                                                                                                                             USA
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                                                                                                                                                                                                                                                                                 COMPOUNDS AND METHODS FOR THE PREVENTION AND
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Pred. No. 7.2e-116;
6; Mismatches 36;
                                                                                                                                                                                                                701 Fifth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 4; Length 359;
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RESULT 13
US-09-072-596-104
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPAX: (206) 682-6031 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 2101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                         APPLICANT:
APPLICANT:
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0
                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                            NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and
                                                                                                                                                                                                           APPLICANT: Hendrich
TITLE OF INVENTION:
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                                                                                                            CITY: Seattle
STATE: Washington
                                                                                                                                            STREET:
                                                                                               COUNTRY:
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                                                                                                                                          6300 Columbia Center,
                                                                                                                                                                                                                                                                                                                                                                                                      Application US/09072596
                                                                                                USA
                                                                                                                                                                                                         Lodes, Michael J.
Hendrickson, Ronald C.
VENTION: COMPOUNDS AND
                                                                                                                                                                                                                                                        Houghton, Raymond
Vedvick, Thomas S.
Twardzik, Daniel R.
                                                                                                                                                                                                                                                                                                        Campos-Neto, Antonia
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Dillon, Davin C.
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   PatentIn Release #1.0,
                                                                                                                                                                SEED and BERRY LLP
                                                                                                                                                                                                                                                                                                                                                         Steven G
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84.2%; Pred. No. 7.26
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                                                                                                                                             701 Fifth Avenue
                                                                                                                                                                                                             METHODS FOR DIAGNOSIS OF
   Version #1.30
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REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 21012
FELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 104:
SEQUENCE CHARACTERISTICS:
LENGTH: 359 amino acide
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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                                                                                                                                                                                             APPLICANT: Houghton, Raymond
APPLICANT: Vedvick, Thomas S.
APPLICANT: Twardzik, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
                                                                                                                                                                                                                                                                                       APPLICANT:
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                                                                                                                                                             NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE: 05-MAY CLASSIFICATION:
                                                                                                                           STREET:
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TOPOLOGY: li
                                                                       COUNTRY:
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Dillon, Davin C.
Campos-Neto, Antonio
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Pred. No. 7.2e-116;
6; Mismatches 36;
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                                                                                                                         Fifth Avenue
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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,112
PILING DATE: 13-MAR-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 31,392
REGISTRATION NUMBER: 31,392
REGISTRATION NUMBER: 31,392
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TELEPHONE: (206) 622-4900
TELEPAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 91:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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APPLICANT:
APPLICANT:
APPLICANT:
         ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                       APPLICANT: Houghton, Raymond
APPLICANT: Vedvick, Thomas S.
APPLICANT: Twardzik, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND
NUMBER OF SEQUENCES: 148
CORRESPONDENCE ADDRESS:
CURRENT APPLICATION DATA:
                                                                                                                               STREET:
CITY: S
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                                                                                                 COUNTRY:
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                                                                                                              Washington
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Dillon, Davin C.
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Pred. No. 3.9e-91;
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APPLICATION NUMBER: US/08/818,111
FILING DATE: 13-MAR-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.417C6
TELECOMMUNICATION INFORMATION:
TELEPAX: (206) 622-4900
TELEPAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 92: SEQUENCE CHARACTERISTICS:
LENGTH: 263 amino acids
TYPE: amino acid
STRANDEDNESS: single
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-818-111-92
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Search completed: November 21, 2003, 17:06:38 Job time : 22 secs
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                                                                                                                                  241 SV 242
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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                    Score
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Match Length DB
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Gapop 10.0 ,
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/cgn2_6/ptodata/1/paa/US07_COMB.pep:*
/cgn2_6/ptodata/1/paa/US087_COMB.pep:*
/cgn2_6/ptodata/1/paa/US082_COMB.pep:*
/cgn2_6/ptodata/1/paa/US082_COMB.pep:*
/cgn2_6/ptodata/1/paa/US083_COMB.pep:*
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/ Ggn2_6/ptodata/1/paa/US100_COMB.pep:*
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/ Ggn2_6/ptodata/1/paa/US103_COMB.pep:*
/ Ggn2_6/ptodata/1/paa/US104_COMB.pep:*
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/cgn2_6/ptodata/1,
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cgn2_6/ptodata/
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   PCT-US99-03265-102
                                Description
Sequence 102, App
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## ALIGNMENTS

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RESULT 1

PCT-US9-03265-102

FOCT-US9-03265-102

FOCT-US9-03265

FOLING DATE: 17-FEB-1999

FOCT-US9-03265

FILING DATE: 135

CLASSIFICATION: 435
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PCT-US99-03268-107
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                                                                                                                                                                                                                                                                                                                         Sequence 107, Application PC/TUS9903268 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Laura A. Coruzzi
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 9532-0023-228
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEPAX: 650-493-5556
                                                                                                                                                                                                                                           APPLICANT: Corixa Corporation
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
NUMBER OF SEQUENCES: 355
                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICATION NUMBER:
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
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                                                                                                               COUNTRY: USA
ZIP: 10036-2811
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                                                                                                                                                                         New York
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                                                                                                                                                   New York
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1155 Avenue of the Americas
                 PatentIn Release #1.0,
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                   Version #1.30
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COUNTRY: USA ZIP: 98104-7092 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk

CITY: Seattle STATE: Washing

Washington

STREET:

6300 Columbia Center,

701 Fifth Avenue

SEED and BERRY LLP

ADDRESSEE:

CORRESPONDENCE ADDRESS:

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US-08-658-800-102
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                                                                                        Sequence 102, Application US/08658800 GENERAL INFORMATION:
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Best Local Similarity
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APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS AND
NUMBER OF SEQUENCES: 123
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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TOPOLOGY: lin
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                      METHODS FOR DIAGNOSIS
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MEDIUM TYPE:

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US-08-659-683-107
US-08-659-683-107
Sequence 107, Application US/08659683
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
NUMBER OF SEQUENCES: 128
CORRESPONDENCE ADDRESS:
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REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 2101:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 682-4900
TELEPAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 102:
SEQUENCE CHARACTERISTICS:
LENGTH: 391 amino acids
TYPE: amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.0%; Score 1949; DB 10; Best Local Similarity 100.0%; Pred. No. 1.7e-155; Matches 391; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/658,800 FILING DATE: 05-7UN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
COMPUTER READABLE FORM:
                                                    STREET: 6300 C
CITY: Seattle
STATE: Washing
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                  COUNTRY: USA
ZIP: 98104-7092
                                                                                                        ADDRESSEE: SEED and BERRY LLP
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                                                  Washington
                                                                                      6300 Columbia Center,
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US-08-680-573-102; Sequence 102, Application US/08680573; GENERAL INFORMATION:
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Best Local 8
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TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 391 amino acids
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/659,683
FILING DATE: 05-JUN-1996
                                                                                                                                                                                                                             APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Neto, Antonia
TITLE OF INVENTION: COMPOUNDS AN
NUMBER OF SEQUENCES: 128
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NAME: Maki, David J.
NAME: Maki, David J.
REGISTANTION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.411C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
COUNTRY: USA
ZIP: 98104-7092
                                                                                                                                ADDRESSEE: SEED and BERRY LLP STREET: 6300 Columbia Center,
                                                                                                    CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
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NAME: Makt, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 2101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 102:
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Matches
                                                                                                                                                                                                          Sequence 107, Application US/08680574 GENERAL INFORMATION:
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APPLICATION NUMBER: US/08/680,573
FILING DATE: 12-JUL-1996
CLASSIFICATION: 435
                                             NUMBER OF SEQUENCES: 133
CORRESPONDENCE ADDRESS:
ANDRESSEE: SEED and BERRY LLP
                                                                                                     APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Neto, Antonio
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 391 amino acids
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 CITY:
STATE:
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STRANDEDNESS: sir
                                  STREET:
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Washington
                                6300 Columbia Center,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 1949; DB 10; ilarity 100.0%; Pred. No. 1.7e-155; Conservative 0; Mismatches 0;
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RESULT 7
US-08-729-622-102
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                                                                                                                                                                                                                      Sequence 102, Application US/08729622 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 391; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 2101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                    APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A
APPLICANT: Dillon, Davin C
APPLICANT: Campos-Neto, An
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APPLICATION NUMBER: US/00
FILING DATE: 12-JUL-1996
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                 TITLE OF INVENTION:
                                                                      APPLICANT:
                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 391 amino acids
TYPE: amino acid
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ZIP: 98104-7092
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Houghton, Raymond
Vedvick, Thomas H.
Twardzik, David R.
TWARTION: COMPOUNDS AND METHODS FOR DIAGNOSIS
NVENTION: TUBERCULOSIS
SEQUENCES: 132
                                                                                                                                  Skeiky, Yasir A.W.
Dillon, Davin C.
Campos-Neto, Antonio
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linear
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CORRESPONDENCE ADDRESS:

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; Sequence 107, Applicati
; GENERAL INFORMATION:
; APPLICANT: Reed, St
; APPLICANT: Réelky,
; APPLICANT: Dillon,
; APPLICANT: Campos-N
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US-08-730-510-107
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Pstentin Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/729,622
FILING DATE: 11-OCT-1996
CLASSIFICATION: 424
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NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 2101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 391 amino acids
TYPE: amino acid
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                                                                                                          Application US/08730510
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               Reed, Steven G.
Skeiky, Yasir A.W.
Dillon, Davin C.
Campos-Neto, Antonio
Houghton, Raymond
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                                                                    Steven G.
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NAME: MAKI, DAVID J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 2101:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 682-6031
INFORMATION FOR SEQ ID NO: 107:
SEQUENCE CHARACTERISTICS:
LENGTH: 391 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.
Best Local Similarity 100.
Matches 391; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION MUMBER: US/08/730,510
FILING DATE: 27-AUG-1996
CLASSIFICATION: 424
CCLASSIFICATION: 424
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APPLICANT: Twardzik, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
NUMBER OF SEQUENCES: 137
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
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ZIP: 98104-7092
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361
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100.0%; Pred. No. 1.7e-155;
tive 0; Mismatches 0;
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391
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RESULT 9 US-08-942-341-102

Sequence 102, Application US/08942341 GENERAL INFORMATION:

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TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MAKI, David J.
NAME: MAKI, David J.
31,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PATENTIN Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF NUMBER OF SEQUENCES: 209
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FILING DATE: 01-OCT-1997
CLASSIFICATION: 435
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                  GQMGARAGGGLSGVLRVPPRPYVMPHSPAAG
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GOMGARAGGGLSGVLRVPPRPYVMPHSPAAG
                                                               LGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAERGPGQMLGGLPV
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Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
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TOPOLOGY:
US-08-942-578-107
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US-08-942-578-107
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/942
FILING DATE: 01-OCT-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 2101
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 391 amino acids
TYPE: amino acid
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
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STATE: Washin
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                LGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAERGPGQMLGGLPV
                                                                                      MVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAMSSLGSSLGSSG
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                                                     MVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAMSSLGSSLGSSG
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E: SEED and BERRY LLP 6300 Columbia Center,
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Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
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Pred. No. 1.7e-155;
D; Mismatches 0;
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US-09-024-753-102
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US-09-024-753-102
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Best Local S
Matches 391
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COMPUTER READABLE FOOM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/024,753
FILING DATE: 18-FEB-1998
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (206) 682-6031 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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APPLICANT:
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REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 21
                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: sir
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MVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAMSSLGSSLGSSG 300
                                                         LLEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN 240
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                                   LLEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN
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Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
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6300 Columbia Center,
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Dillon, Davin C.
                                                                                                                                                                                                                                                                                                                       100.0%; Score 1949; DB 14; ilarity 100.0%; Pred. No. 1.7e-155; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                        Length 391;
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                                                                                                                                                                                                              Matches 391;
                                                                                                                                                                                                                                 Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICANT: Twardzik,
APPLICANT: Lodes, Mid
TITLE OF INVENTION: 0
TITLE OF INVENTION: 1
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
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CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                      TYPE:
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                                                                    SSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI
                                                                                                                                        MVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG
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Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
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                                                                                                                                                                                                             100.0%; Score 1949; DB 14; ilarity 100.0%; Pred. No. 1.7e-155; Conservative 0; Mismatches 0;
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Dillon, Davin C.
Campos-Neto, Antonio
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US-09-072-967-107
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ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/09/072,967
FILING DATE: 05-MAY-1998
CLASSIFICATION: TARKERS OF 
                                                                                                                                      Matches
                                                                                                                                                                  Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 13
SEQUENCE CHARACTERISTICS:
LENGTH: 391 amino acids
TYPE: amino acid
STERANTEDERSCS.
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NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 2101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
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APPLICANT: Lodes, Michael J.
APPLICANT: Hendrickson, For Invention: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
OUTBER OF SEQUENCES: 355
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MVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG
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Vedvick, Thomas S.
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                                                                                                                           100.0%; Score 1949; DB 14; 100.0%; Pred. No. 1.7e-155; tive 0; Mismatches 0;
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; OTHER INFORMATION: MTB39 (TbH9) protein full-length
US-09-597-796C-8
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PRIOR APPLICATION NUMBER: WO PCT/US99/07717
PRIOR APPLICATION NUMBER: WO PCT/US99/07717
PRIOR FILING DATE: 1999-04-07
PRIOR FILING DATE: 1999-04-07
PRIOR APPLICATION NUMBER: US 60/158,338
PRIOR FILING DATE: 1999-10-07
PRIOR APPLICATION NUMBER: US 60/158,425
PRIOR FILING DATE: 1999-10-07
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                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn Ver. 2
SEQ ID NO 8
LENGTH: 391
                                                                                                                                                                                                           Matches 391;
                                                                                                                                                                                                                               Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/597,796C
CURRENT FILING DATE: 2000-06-20
PRIOR APPLICATION NUMBER: US 09/056,556
PRIOR FILING DATE: 1998-04-07
PRIOR APPLICATION NUMBER: US 09/223,040
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APPLICANT: Reed, Steven
APPLICANT: Alderson, Mark
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
FILE REFERENCE: 014058-009050US
                                                                                                                                                                                                                                                                                                                                          ORGANISM: Mycobacterium tuberculosis
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Pred. No. 1.7e-155;
Mismatches 0;
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PRIOR APPLICATION NUMBER: US 60/158,425
PRIOR FILING DATE: 1999-10-07
NUMBER OF SEQ ID NOS: 202
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 26
LENGTH: 391
TYPE: PRT
ORGANISM: Mycobacterium tuberculosis
FEATURE:
OTHER INFORMATION: TDH9 (Mtb39A)
US-09-688-672A-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Skeiky, Yasir
APPLICANT: Reed, Steven
APPLICANT: Houghton, Raymond L.
APPLICANT: Houghton, Raymond L.
APPLICANT: McNeill, Patricia D.
APPLICANT: Dillon, Davin C.
APPLICANT: Lodes, Michael L.
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
FILE REFERENCE: 014058-009041US
CURRENT APPLICATION NUMBER: US/09/688,672A
CURRENT FILING DATE: 2000-10-10
PRIOR APPLICATION NUMBER: US 60/158,338
PRIOR FILING DATE: 1999-10-07
PRIOR FILING DATE: 1999-10-07
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US-09-688-672A-26
; Sequence 26, Application US/09688672A
; GENERAL INFORMATION:
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Search completed: November 21, 2003, 17:09:44
Job time: 174 secs

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Result
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    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.
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    1 MVDFGALPPEINSARMYAGP.....SGVLRVPPRPYVMPHSPAAG
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Y892_MYCTU
Y102_MYCTU
Y442_MYCTU
Y878_MYCTU
Y878_MYCTU
Y878_MYCTU
SRA_MYCLE
Y096_MYCTU
Y118_MYCTU
YU21_MYCTU
YU21_MYCTU
YY29_MYCTU
ELS MOUSE
ELS MOUSE
YY26_MYCTU
ELS HUMAN
ELS HUMAN
A180 HUMAN
FRY3_YEAST
A180 HUMAN
ICPO HSV2H
STFR_ECOLI
N214 HUMAN
N214 HUMAN
V236_BWML_PIG
SAMU_PIG
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Q107297 mycobacteri
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O50703 mycobacteri
P54320 mus musculu
Q50702 mycobacteri
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Q50702 mycobacteri
Q9372 rattus norv
P15502 homo sapien
P47033 saccharomyc
C60641 homo sapien
P47032 escherichia
P36072 escherichia
P36073 mycobacteri
Q9fec4 chlamydomon
P52172 drosophila
P24856 notothenia
Q10169 schizosacch
Q24523 drosophila
P34521 drosophila
P34511 mesocricetu
Q50597 mycobacteri
P71789 mycobacteri
P71789 mycobacteri
P04893 saccharomyc
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Q10813 mycobacteri
O53951 mycobacteri
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## ALIGNMENTS

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STRAIN=CDC 1551 / Oshkosh; Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L., Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A., Bishai W., "Whole genome comparison of Mycobacterium tuberculosis clinical and laboratory strains."; Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases!- SIMILARITY: BELONGS TO THE MYCOBACTERIAL PPE FAMILY.  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).  EMBL; Z7555; CAA99966.1; EMBL; Z7555; CAA99966.1; EMBL; AE007013; AAK45669.1; PIR; H70741; H70741. TIGR; MT106; Thberculist; Rv1361c; InterPro; IPR000030; Microbac_PPE.	1 6

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Q10813;
01-OCT-1996
15-DEC-1998
16-OCT-2001
                                                                                                                                    MEDLINE=98295987; PubMed=9634230; Garnier T., Churcher C., Harris Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-1996 (Rel. 34, Created)
15-DEC-1998 (Rel. 37, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
Hypothetical PPE-family protein Rv289;
RV2892C OR MT2959 OR MTCY274.23C.
           SEQUENCE FROM N.A.

STRAIN-CDC 1551 / Oshkosh;

Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Fleischmann R.D., Alland D., Eisen J.A., Haft D., Hickey E., Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg Kolonay J.F., Nelson W.C., Weidman J., Khouri H., Gill J., Mikula
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18; Mismatches
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RESULT 3
Y102 MYCTU STANDARD; PRT; 463 AA.
ID 7102 MYCTU STANDARD; PRT; 463 AA.
AC 053951;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-CCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical PPE-family protein Rv1802.
GN RV1802 OR MT1851 OR MTV049.24.
OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinobacteriaceae; Mycobacteri

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Hypothetical protein;
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Submitted (APR-2001) to
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EMBL; AE007119; AAK47285.1; -
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Pfam; PF00823; PPE; 1.
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between the Swiss Institute of Bioinformatics and the EMBL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VATNFFGQNTPAIAATEAQYAEMWAQDAAAMYAYAGSAAIAT-ELTPFTAAPVTTSPAAL
                                                     VPPRPYVMPHSPAAG
                                                                                                                VPPDWAARARWANPAAWRLPGDDVTALRGTAENA---LLRGFPMASAGQSTGGGF--VHK
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                                                                                                                                                                                                                                                                                                                                                                                                     --GGLWKTVSPHRSPISNMVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAA
                                                                                                                                                                                                                            GPRÁSPSVAGGGAVGGVQTPQPYWYWALDRESIGGSVSAALGKGSSAGSLS
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41.8%;
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                                                        391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47;
                                                                                                                                                                                                                                                                                                                                             ----LQFEASLAQQAIPGTPGGAG--DSGSSVLDSWGPTIFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 705; DB 1;
Pred. No. 4.4e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3E3D1F20D7827199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        134;
                                                                                                                                                                                                                                                                                    --SGLGGGVAANLGRAASVGSLS
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Best Local S
Matches 174
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STRAIN=CDC 1551 / Oshkosh;

Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,

Fleischmann R.D., Alland D., Gwinn M.L., Haft D., Hickey E.,

Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,

Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg;

Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-98295987; PubMed=9634230;
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C.E., Tekaia F., Bardocok K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein; Complete proteome. CONFLICT 401 401 S -> L (IN SEQUENCE 463 AA; 46021 MW; EE64828BF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TubercuList; Rv1802; -...
InterPro; IPR000030; Microbac_PPE.
Pfam; PF00823; PPE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE MYCOBACTERIAL PPE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AL022021; CAA17723.1; EMBL; AE007044; AAK46123.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TIGR; MT1851; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Whole genome comparison of Mycobacterium tuberculosis clinical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                IATNILGQNTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATILLPFEEAPEMTSAGGI
                                                                                                                                                                                                                                                                                         SAGLMVAAASPYVAMMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMIL
                                                                                                                                                                                                                                                                                                                                       MDFGVLPPEINSGRMYAGPGSGPMLAAAAAMDGLATELQSTAADYGSVISVLT-GVWSGQ
                                   NSMLGLGFAESKMVLPANDTVISTIFGMVQFQKFFNPVTPFNPDLIPK---
                                                                                                                                               LEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVS--PHRSPI-
                                                                                                                                                                                     AATNIFGONTGAIAAAEARYAEMWAQDAAAMYGYAGSSSVAT-QVTPFAAPPPTTNAAGL
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                                                                                                                                                                                                                                                                                                                                                                            VDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIGS
                                                                                                              ATOGVAVAQAVGASAGN-ARSLVSEVLEFLA--TAGTNYNKTVASLMNAVTGVPYASSVY
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ilarity 42.8%;
Conservative 4
                                                                        SIMVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVRA
·SSGLGG----GVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPL
                                                                                                                                                                                                                                                                                                                                                                                                                      48;
                                                                                                                                                                                                                                                                                                                                                                                                                  Score 688.5; DB 1;
Pred. No. 4.5e-33;
8; Mismatches 136;
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EE64828BF09FA551 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                    136; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 463;
                                                                                                                                                                                                                                                                                                                                                                                                                    49;
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RESULT 4
Y442_MYCTU
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                                                                                                                                                                       between the Swiss Institute of Bioinformat
the European Bioinformatics Institute. The
use by non-profit institutions as long
modified and this statement is not removed.
entities requires a license agreement (See
or send an email to license@isb-sib.ch).
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01-NOV-1995 (Rel. 32, Created)
16-OCT-2001 (Rel. 40, Last sequence upda
16-OCT-2001 (Rel. 40, Last annotation up
Hypothetical PPE-family protein Rv0442c.
RV0442C OR MT0458 OR MTV037.06C.
                                                                                                                                                                                                                                                                                                                     laboratory strains.";
Submitted (APR-2001) to
-!- SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Fleischmann R.D., Alland D., Gwinn M.L., Haft D., Hickey E.,
Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg
Belcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula
                                                                                     EMBL; M15467; AAA88235.1; ALT_INIT.
EMBL; AL021932; CAA17399.1; -.
EMBL; AE006948; AKK44681.1; -.
PIR; C70830; C70830.
                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
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                                                                   PIR; C70830; C70830
TIGR; MT0458; -
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InterPro; IPR000030; Microbac PPE.
InterPro; IPR002989; Mycobac pentapep.
Pfam; PF01469; Pentapeptide_2; 5.
                                                    TubercuList; Rv0442c;
                                                                                                                                                                                                                                                                                                                                                                           Whole genome comparison of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               he 65-kilodalton antigen of Mycobacterium tuberculosis.";
Bacteriol. 169:1080-1088(1987).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGLQAVPAAAISEGSLLSQMALASVAGGALGGAAARATGGFLGGGRV
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                                                                                                                                                                                                                                                                                                                     the EMBL/GenBank/DDBJ databases. TO THE MYCOBACTERIAL PPE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                           Mycobacterium tuberculosis
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                                                                                                                                                                                                           Usage
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RESULT 5
Y878 MYCTU
ID Y878 MYCTU
ID Y878 MYCTU
AC Q10540;
DT 01-0CT-1996 (
DT 01-0CT-2001 (
DE Hypothetical
GN RV0878C OR RV10878C OR RV10878C OR RV10878C OR RV10878C OR RV10878C OR C COrynebacterion
OC Bacteria; Act
OC Corynebacterion
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SEQUENCE 48
                                                   MEDLINE=98295987; PubMed=9634230;
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Badcock K., Beylin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
16-OCT-2091 (Rel. 40, Last annotation update)
Hypothetical PPE-family protein Rv0878c.
RV0878C OR MT0901 OR MTCY31.06C.
                                                                                                                                                                                                                                                                                                                                                                     STRAIN=H37Rv;
                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
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G -> GNNNIG (IN REF.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Whole genome comparison of Mycobacterium tuberculosis clinical laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=CDC 1551 / Oshkosh;
FleisChmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long a modified and this statement is not removed. entitles requires a license agreement (See lor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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TubercuList; Rv0878c;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       between the Swiss Institute of Bioinformatics and the EMBL outst
the European Bioinformatics Institute. There are no restrictions
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    -I- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
    -I- SIMILARITY: BELONGS TO THE MYCOBACTERIAL PPE FAMILY.

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STRAIN=CDC 1551 /
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PF00823; PPE; 1.
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                        RALPLTSLTSAAERGPGQMLGGL--PVGQMGARAGGGLSG
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                                                                          QTAAQNGVRAMSSLGS-SLGSSGLGGGVAA--NLGRAASVGSLSVPQAWAAANQAVTPAA
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IPR002989; Mycobac pentapep
1469; Pentapeptide_2; 4.
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POTENTIAL.
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Pred. No. 5.8
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4 X 10 AA APPROXIMATE REPEATS.
5 C58BEC607F0675E2 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-98295987; PubMed=9634230; Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Badcock K., Beylin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence."; Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboratio between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no wall modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg
Delchei M., Utterback T., Weidman J., Khouri H., Gill J., Mikula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MYCTU
                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF01469; Pentapeptide_2; 11. Pfam; PF00823; PPE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         laboratory strains.";
Submitted (APR-2001) to the
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TIGR; MT1599; -.
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                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Whole genome comparison of Mycobacterium tuberculosis clinical
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SAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMIL
                                                          MNFSVLPPEINSALMFAGAGPGPMLAAASAWTGLAGDLGSAAASFSAVTSQLATGSWQGP
                                                                                                              VDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIGS
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IPR002989; Mycobac_pent;
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66736
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48; Mismatches
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209F1593D52533A2 CRC64;
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9e-17;
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Q07297;
Q1-NOV-1995
Q1-NOV-1995
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                      MEDINES: NESSITION N.R., Parkhill J., James K.D., Thomson N.R., Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R., Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D., Wheeler R.R., Honore N., Garnier T., Chillngworth T., Connor R., Mungall K., Basham D., Brown D., Chillngworth T., Connor R., Mungall K., Bevin D., Jagels K., Lacroix C., Maclean J., Moule S., Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Mulle S., Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M., Ruther S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
                                                                                                                      This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no resti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vega-Lopez F., Brooks L.A., Dockrell H.M., de Smet K.A.L., Thompson J.K., Hussain R., Stoker N.G.; "Sequence and immunological characterization of a serine-rich antigen from Mycobacterium leprae."; Infect. Immun. 61:2145-2153(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SRA OR ML0411 OR MLCL383.14.
Mycobacterium leprae.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                            "Massive gene decay in the leprosy bacillus."; Nature 409:1007-1011(2001).
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MEDLINE=95020554; PubMed=7934845;
                                                                                                                                                                                                                                                                                                                                         Squares S., S
Barrell B.G.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rinke de Wit T.F., Clark-Curtiss J.E., Abebe F., Kolkon A.H.J., Jonson A.A.M., Thole J.E.R.;
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(Rel. 40, Last annotation update)
antigen (25L) (45 kDa protein).
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PIR; S33522; S33522.
PIR; S39872; S39872.
Leproma; ML0411; -.
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SEQUENCE
                                       _MYCTU STANDARD; PRT; 463 AA. Q10892; O1-OCT-1996 (Rel. 34, Created) O1-OCT-1996 (Rel. 34, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Hypothetical PPE-family protein Rv0096.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U00015; AAC43220.1; --
EMBL; X68431; CAA46480.1; --
EMBL; Z21952; CAA79950.1; --
EMBL; Z97179; CAB09938.1; --
EMBL; AL583918; CAC29919.1;
                   Mycobacterium tuberculosis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
          Corynebacterineae; Mycobacteriaceae;
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NCBI_TaxID=1773;
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S -> L (IN REF. 2).
H -> D (IN REF. 2).
P -> L (IN REF. 2).
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                                                                                                                                                                                                                                                                                                                       TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-CDC 1551 / Oshkosh; Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., Hickey E., Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg Kolonay J.F., Nelson W.C., Umayam J., Khouri H., Gill J., Mikula Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Whole genome comparison of Mycobacterium tuberculosis c
laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-i- SUBCELLULAR LOCATION: Integral membrane protein (Pot-
-i- SIMILARITY: BELONGS TO THE MYCOBACTERIAL PPE FAMILY.
                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                               TIGR, MT0105;
Tuberculist; Rv0096;
InterPro; IPR000030; Microbac_PPE.
Pfam; PF00823; PPE; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
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SEQUENCE FROM N.A.
STRAIN=H37RV;
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                  AAVEEASDT - - - -
                                               FFGINTVPIALNEADYVRMWLQAADTMAAYQAVADAATVAVPSTQPAPPIRAPGG-----
                                                                           LLGQNTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATALLPFEEAPEMTSAGGLLEQA
                                                                                                              YVAAHGPYLAWLEQTAINSAVTAAQHVAAAAAYCSALAAMPTPAELAANHAIHGVLIATN
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POTENTIAL.
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Pred. No. 4.8e-12;
4; Mismatches 144
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DE HYPOth
GN RV3018
OS MYCODA
OC COTYNE
OX NCBLT
RN STRAIN
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SEQUENCE FROM N.A.
STRAIN-CDC 1551 / Oshkosh;
STRAIN-CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White U., Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E., Peterson J., DeBoy R., Dodson R., Ermolaeva M.D., Salzberg S.L.
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.
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Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Badcock K., Beylin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=Isolate 50410;
STRAIN=Isolate 50410;
Bratki A.H., Dale J.W.;
Submitted (APR-1991) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE MYCOBACTERIAL PPE FAMILY.
-!- CAUTION: In strain Oshkosh the gene for this protein interrupted in position 307 by an IS6110 element.
-!- CAUTION: Was originally (Ref.3) thought to be a dihyd
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P3150; O53265;
01-JUL-1993 (Rel. 26, Created)
16-OCT-2001 (Rel. 40, Last sequence updated)
28-FEB-2003 (Rel. 41, Last annotation upon the sequence of the sequen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mycobacterium tuberculosis.
Bacteria; Actinobacteria; Actinobacteridae; Actinor
Corynebacterineae; Mycobacteriaceae; Mycobacterium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 160-374 FROM
                                                                                                                                                                                                                                                                                                                                   CAUTION: Ref.3 sequence differs in positions 294; 337 and 355.
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TIGR; MT3098; -.
TIGR; MT3101; -.
MEDLINE-9825587; PubMed=9634230; Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F. Badcock K., Basham D., Brown D., Chillingworth T., Connor R. Badries R., Devlin K., Feltwell T., Gentles S., Hamlin N., H. Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murph Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
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053268; 053269;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical PPE-family protein Rv3021c/Rv3022c.
RV3021C/RV3022C OR MT3106 OR MTV012.35C/MTV012.36C.
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Pred. No. 4.7e-12;
6; Mismatches 178
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Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases
-i- SIMILARITY: BELONGS TO THE MYCOBACTERIAL PPE FAMILY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
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EMBL; AL021287; CAA16107.1; ALT_FRAME.
EMBL; AE007129; AAK47435.1; -._
TIGR; MT3106; -.
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GOMGARAGGGLSGV
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L -> V (IN REF. 2).
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Pred. No. 6.6e-12;
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Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harcoler S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harcoler S., Edward C.E. III, Tekaia F., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Gordon S.V., Basham D., Brown D., Chillingworth T., Connor R., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Holre Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L. Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
Nature 393:537-544(1998).
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Pfam; PF00823; PPE; 1.
Hypothetical protein; Complete pro
SEQUENCE 178 AA; 19811 MW. and
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16-OCT-2001 (Rel. 40, Last sequence upolicy of the correction of the co
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STRAIN=CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D
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Submitted (APR-2001) to
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Kolonay J.F., Nelson W.C., Umayam L.A., Ermol
Delcher A., Utterback T., Weldman J., Khouri
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Bacteria, Actinobacteridae, Actinomycetales,
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                                                                            IPAEYISNIIYEGPGADSLSAAAEQLRLMYNSANMTAKSLTDRLGELQE-----NWK
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19811 MW; 8BE1FC025ABFBEA6 CRC64;
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Gwinn M.L., Haft D., Hickey
L.A., Ermolaeva M.D., Salzbe
J., Khouri H., Gill J., Miku
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complete genome sequence.";
Nature 393:537-544(1998).
-!- SIMILARITY: BELONGS TO THE MYCOBACTERIAL PPE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical PPE-family protein Rv3425.
RV3425 OR MTCY78.04C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MYCTU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical SEQUENCE 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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Q50703;
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AGVNTPAIADLDAQYDQYRARNVAVMNAYVSWTRSALSDLPRWREPPQIYRGG
                                                       LGONTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATLLPFEEAPEMTSAG 179
                                                                                                                  ADAVERYLQWLSKHSSQLKHAAWVINGLANAYNDTRRKVVPPEEIAANREERRRLIASNV
                                                                                                                                                                      VAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMILIATNL
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176 AA; 1
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9855 MW; B8CEF2E9463B87B0 CRC64;
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RESULT 13
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SEQUENCE
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P54320;
01-OCT-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=BALB/c; TISSUE=Lung;
MEDLINE=95130069; PubMed=7829060;
Mydner K.S., Sechler J.L., Boyd C.D., Passmore H.C.;
"Use of an intron polymorphism to localize the tropoelastin mouse chromosome 5 in a region of linkage conservation with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El the European Bioinformatics Institute. There are no resti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- FUNCTION: MAJOR STRUCTURAL PROTEIN OF TISSUES SUCH AS AORTA /
NUCHAL LIGAMENT, WHICH MUST EXPAND RAPIDLY AND RECOVER COMPLI-
-!- SUBUNIT: THE POLYMERIC ELASTIN CHAINS ARE CROSS-LINKED TOGET!
INTO AN EXTENSIBLE 3D NETWORK.
-!- SUBCELLULAR LOCATION: EXTRACELLULAR MATRIX OF ELASTIC FIBERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHAIN
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Genomics 23:125-131(1994).
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Mammalia; Eutheria;
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15-SEP-2003
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1996 (Rel. 34, Last sequence update)
2003 (Rel. 42, Last amotation update)
precursor (Tropoelastin).
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                                                 LMNNVPQALQQLAQPTQGT---
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LGAGVPGFGAGAGVPGFGAGAGVPGFGAGAGVPGFGAGAVPGSLAASKAAK
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Rodentia;
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AERGP ---

MYCTU

Q50702;

YY26\_MYCTU

STANDARD;

Created)

01-NOV-1997 (Rel. 35, Last seque 16-OCT-2001 (Rel. 40, Last annot Hypothetical PPE-family protein RV3426 OR MTCY78.03C.

Mycobacterium tuberculosis

NCBI\_TaxID=1773;

MEDLINE=98295987; SEQUENCE FROM N.A.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harr. Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroy. Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence."; Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00823; PPE; 1.

Hypothetical protein; Complete proteome.

SEQUENCE 232 AA; 25872 MW; D76512D49EB272C6 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Corynebacterineae; Mycobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000030; Microbac_PPE
                                                                                                                            VAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMILIATNL 126
                                                                            ADAALRYLDWLSKHSRQILRTARVIESLVMAYEETLLRVVPPATIANNREEVRRLIASNV
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                                                                                                                                                                                                                              LPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIGSSAGLM
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                                                                                                                                                                              IPAEYISNVIYEGPRADSLYAADQRLRQLADSVRTTAESLNTTLDELH-ENWKGSSSEWM
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Last annotation update)
ly protein Rv3426.
                                                                                                                                                                                                                                                                              Score 151.5; DB Pred. No. 0.022; 8; Mismatches
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THE RESULT OF THE PERSON AND THE PER
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ELS_RAT
Q99372;
01-OCT-1996
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15-SEP-2003
Elastin prec
  EMBL;
                                                                                               the European Bioinformatics Institute. There are no rest
use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by ar
entitles requires a license agreement (See http://www.isb-
or send an email to license@isb-sib.ch).
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-i- FUNCTION: MAJOR STRUCTURAL
NUCHAL LIGAMENT, WHICH MUST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=92241859; PubMed=1572637;
Pierce R.A., Alatawi A., Deak S.B., Boyd C.D.;
"Elements of the rat tropoelastin gene associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Deak S.B., Pierce R.A., Belsky S.A., Riley D.J., Boyd "Rat tropoelastin is synthesized from a 3.5-kilobase J. Biol. Chem. 263:13504-13507(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=91104868; PubMed=1702999; Pierce R.A.; Deak S.B., Stolle C.A., "Heterogeneity of rat tropoelastin m Biochemistry 29:9677-9683(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10116;
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       splicing."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 781-864 FROM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: MAJOR STRUCTURAL PROTEIN OF TISSUES S NUCHAL LIGAMENT, WHICH MUST EXPAND RAPIDLY AND SUBUNIT: THE POLYMERIC ELASTIN CHAINS ARE CROSS INTO AN EXTENSIBLE 3D NETWORK.
SUBCELLULAR LOCATION: EXTRACELLULAR MATRIX OF E
                                                                                                                                                                                                                                                                                                              PTM: THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALTERNATIVE rocurrential confirmation
M60647;
J04035;
M86372;
                                                                                                                                                                                                                                                                                                                                                                                  IsoId=Q99372-7; Sequence=VSP_004244, VSP_004246;
                                                                                                                                                                                                                                                                                                                                                                                                                                       IsoId=Q99372-6;
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                                                                                                                                                                                                                                                                                                        IsoId=Q99372-8; Sequence=VSP_004244, VSP_004245, M: THE CROSSLINKS ARE MADE OF DEAMINATED LYS.
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2003 (Rel. 42, Last annotation update)
precursor (Tropoelastin) (Fragment).
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  AAA42269.1;
AAA42268.1;
AAA42271.1;
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PubMed=2971041;
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Sciurognathi; Muridae;
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64 67 Matches Query Match Best Local

43;

Conservative

18;

Similarity

7.8%; 35.2%;

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PIR; G70738; G70738. TubercuList; Rv3426;

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Job time : 20 secs
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Best Local Simi
Matches 102;
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EMBL; M86363; AAA42271.1; JOINED.
EMBL; M86364; AAA42271.1; JOINED.
EMBL; M86366; AAA42271.1; JOINED.
EMBL; M86371; AAA42271.1; JOINED.
EMBL; M86376; AAA42272.1; JOINED.
EMBL; M86373; AAA42272.1; JOINED.
EMBL; M86373; AAA42272.1; JOINED.
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VARSPLIC 263 307
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PRINTS; PR01500; TROPOELASTIN.
Structural protein; Connective tissue; Repeat; Signal;
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                                                                            342 SLTSAAERGPGQMLGGLPVGQMGARAG-GGLSGV 374
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                                                                                                                                 SLGSSLGSSGLGGGV-----AANLGRAASV---GSLSVPQAWAAANQAVTPAARALPLT 341
                                                                                                                                                                                      PHRSPISNMVSMANNHMSMTNSGVSM-TNTLSSMLKGF-APAAAAQAVQTAAQNGVRAMS 290
                                                                                                                                                                                                                  SAGGLL----EQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSS-KLGGLWKTVS 232
                                                                                                                                                                                                                                                                        -----GAGTLGGLVPG-----AVPGALPGAVPGALPGAVPGALP-GAVPGVP
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           2003, 17:04:39
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;; Pred. No. 0.11;
31; Mismatches 153
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ELASTIN.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Missing (In isoform 4, isoform 6, 7 and isoform 8).
/FTId=VSP_004246.
; 456894BB09E79FD4 CRC64;
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EMBL; AE007000; AAK45;
TIGR; MT1234; -.
TubercuList; Rv1196;
InterPro; IPR000030; Microbac PPE. InterPro; IPR000508; SigFTase. Pfam; PF00823; PPE; 1. PROSITE; PS00501; SPASE I 1; 1. SEQUENCE 393 AA; 39688 MW; 86F
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submitted (APR-2001) to the
EMBL; AE007161; AAK47941.1;
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STRAIN=CDC 1551 / Oshkosh;
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Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzbe
Kolonay J.F., Utterback T., Weidman J., Khouri H., Gill J., Miku
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Mycobacterium tuberculosis.
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Best Local Simi
Matches 335;
                                                                                                                                                                                                                                           MEDLINE=98295987; PubMed=9634230;

A COLE S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harr A Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., A Badcock K., Basham D., Brown D., Chillingworth T., Connor R., A Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroy A Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., A Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., A Rutter S., Seeger K., Skelton S., Squares S., Squares R., B Rutter S., Seeger K., Whitehead S., Barrell B.G.;

T "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";

Nature 393:537-544(1998).
                       Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mycobacterium tuberculosis.
Bacteria; Actinobacteria; Actinobacte
Corynebacterineae; Mycobacteriaceae;
                                                                                                   Hypothetical SEQUENCE 3:
                                                                                                                                                                                                 EMBL; Z95390; CAB08702.1; -. TubercuList; Rv3478; -.
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PF00823; PPE; 1.
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393 AA; 39413 MW;
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Pred.
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No. 4.3e-84;
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                                   laboratory strains.";
Submitted (APR-2001) to the
EMBL; AL022021; CAA17711.1;
EMBL; AB007043; AAK46108.1;
TIGR; MT1838;
                                                                                                                                                                                                                                                                                                    MBDLINE-98295987; PubMed=9634230; Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Biglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence."; Nature 393:537-544(1998).
                                                                                                                                                                 SEQUENCE FROM N.A.

STRAIN-CDC 1551 / Oshkosh;

Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,

Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., Hickey E.,

Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E.,

Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.

Belcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mycobacterium tuberculosis.
Bacteria, Actinobacteria, A
Corynebacterineae, Mycobact
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01-MAR-2002 (TrEMBLrel.
01-OCT-2002 (TrEMBLrel.
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RV1789 OR MT1838 OR MTV049.11.
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                       TubercuList; Rv1789;
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 Microbac_PPE
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Matches 177
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Best Local S
Matches 179
                                                                                                                                                                                                                           InterPro; IPR00
Pfam; PF00823;
SEQUENCE 410
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Complete proteome.
SEQUENCE 411 AA;
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Q99QII;
01-JUN-2001 (TrEMBLrel. 17, C
01-JUN-2001 (TrEMBLrel. 17, L
01-OCT-2002 (TrEMBLrel. 22, L
Rv1808-like protein.
MYC1808 OR OV1808.
                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
SETRAIN=myc 94-2272, and OV254;
SITRAIN=myc 94-2272, and OV254;
Sivadon V., Heym B., Mazancourt P., Gaillard J
"PPE Rv1808 orthologue of Mycobacterium microt
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ
EMBL; AF335180; AAK20894.1; -.
EMBL; AF33519; AAK20893.1; -.
InterPro; IPR000030; Microbac_PPE.
InterPro; IPR000030; Microbac_PPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mycobacterium microti.
                       SSAGLMVAAASPYVAMMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI
                                                                                  MVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QNGVRAMSSLGSSLGSSGLGGGGVAANLGRAASVGSLSVPQAWAA-ANQAVTPAARALPLT
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PSSITMAAAVAPYVAWISVTAGQAEQAGAQAKIAAGVYETAFAATVPPPVIEANRALLMS
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                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                     40044 MW;
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44.5%; Pred. No. 2e-34;
tive 51; Mismatches 1
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Last annotation update)
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Pred. No. 7.6
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053957;
01-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=98295987; PubMed=9634230; Gornier T., Churcher C., Harris Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McJean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence."; Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O. Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=CDC 1551 / Oshkosh; Fleischmann R.D., Alland D., Eisen J.A.,
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STRAIN=H37Rv;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
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RV1808 OR MT1856.1 OR MTV049.30.
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                                                                                                                                                                                                                                                                                      laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ
EMBL; AL022021; CAA17729.1; -.
EMBL; AE007044; AAK46129.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                     "Whole genome comparison of
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                                                                                                                                                                          Pro; IPR000030; PF00823; PPE; :
                                                                                                                                                                                                                                                              MT1856.1;
                                Similarity
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                                                                                                                    409
  Conservative
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                                                                                                                 ΑA;
                             38.5%;
                                                                                                                    39917
                                                                                                                                                                                                     Microbac_PPE
                                                                                                                    WW;
  Score 751; DB
Pred. No. 2.9e
53; Mismatches
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                                                                                                                                                                                                                             STRAIN=CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eiser
Fleischmann R.D., Alland D., Eiser
Roterson J., DeBoy R., Dodson R.,
Kolonay J.F., Nelson W.C., Umayam
Delcher A., Utterback T., Weidman
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01-JUN-1998 (TrEMBLrel:
01-OCT-2002 (TrEMBLrel:
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RV1807 OR MT1856 OF
                                                                                                              laboratory strains.";
Submitted (APR-2001) to the
                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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AE007044; AAK46128.1;
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odson R., Gwinn M., Haft D., Hickey
, Umayam L.A., Ermolaeva M., Salzbo
, Weidman J., Khouri H., Gill J., Mi
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CONFLICT 227 2:
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O1.-JUN-1998 (TrEMBLrel. 06, Created)
O1.-JUN-1998 (TrEMBLrel. 06, Last sequence update)
O1.-JUN-1998 (TrEMBLrel. 22, Last annotation update)
PPE-family protein (PPE family protein).
RV1801 OR MTW049.23 OR MT1850.
                    MEDLINE-9829987; PubMed=9634230; Garnier T., Churcher C., Harris Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Gardon S.V., Basham D., Brown D., Chillingworth T., Connor R., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Chillingworth T., Connor R., Jayles K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence."; Nature 393:537-544(1998).
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Bacteria; Actinobacteria; Actinobacteridae; Actinor
Corynebacterineae; Mycobacteriaceae; Mycobacterium
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403 AA;
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238 V
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V -> L (IN REF. 2).
U DCE18880FD15CBFE CRC64;
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Best Local S
Matches 182
                                                                                                                                                                                              Q9Z5KO PRELIMINARY; PRT; 421 AA. Q9Z5KO; 01-MAY-1999 (TrEMBLrel. 10, Created) 01-MAY-1999 (TrEMBLrel. 10, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update Putative PPE protein (PPE-family protein). MLI1182 OR MLCB1701.08C.
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Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula
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Submitted (APR-2001) to the
EMBL; AL022021; CAA17722.1;
EMBL; AE007044; AAK46122.1;
                                                                                             Corynebacterineae;
NCBI_TaxID=1769;
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                                                                                                                                                      Mycobacterium leprae. Bacteria; Actinobacteridae;
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Tuberculist; RV1801; -.
Tuberculist; RV1801; Microbac_PPE.
MEDLINE=21128732; PubMed=11234002;
                                                SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Complete proteome
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fam; PF00823; PPE;
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                                                                                                                           Mycobacteriaceae;
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Pred. No. 2.1e-33;
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                                                                                                                           Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -AAERGPGQMLGGLPVGQMGARAGGGLSGVLR
                                                                                                                                                        Actinomycetales;
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1 A.,
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P96362
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Best Local S
Matches 174
                                                                                                                                                                                                             P96362; PRELIMINARY; PRT; 391 AA.
P96362;
01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical 38.1 kDa protein (PBE family protein).
RVI039C OR MTCY10G2.10 OR MTI068.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R., Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D., Mungall K., Basham D., Brown D., Chillingworth T., Connor R., Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S. Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M. Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
SEQUENCE FROM N.A.
STRAIN=H37Rv;
MEDLINE=98295987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Massive gene decay in the leprosy Nature 409:1007-1011(2001).
EMBL; AL049191; CAB39148.1; -.
EMBL; AL583921; CAC31563.1; -.
                                                                                                     NCBI_TaxID=1773;
                                                                                                                                  Bacteria; Actinobacteria;
Corynebacterineae; Mycobac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00823; PPE; Complete proteome.
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Barrell B.G.;
                                                                                                                                                                                     Mycobacterium tuberculosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAAQAVQTAAQNGVRAMSSLGSSLGSSGLGGGVAANLGRAASVGSLSVPQAWAAANQAVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    L------VPQALQQ-----LAQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LIATNILGQNTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATATLLPFEEAPEMTSAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TQGTTPSSKLGG--LWKTVSPHRSPISNMVSMANNHMSMTNSGVSMTNTLSSMLKGFAPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QTAVPDSSSAAAPQLWGGFAQHLSPINDTLSMINNHAGMANAGLSLVNGMGSAMKSLAP-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      421
        PubMed=9634230;
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41.1%;
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                                                                                                                                Actinobacteridae; Actino
cteriaceae; Mycobacterium
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5; Mismatches
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Pred. No. 3
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.9e-33;
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                                                                                                                                                                Actinomycetales;
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Best Local Simi
Matches 166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fleischmann R.D., Alland D., Eisen J.A., Peterson J., DeBoy R., Dodson R., Gwinn M. Kolonay J.F., Nelson W.C., Umayam L.A., E Delcher A., Utterback T., Weidman J., Khon Bishai W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Gordon S.V., Biglmeier K., Gas S., Barry C.E. III, Tekaia F. Badcock K., Basham D., Brown D., Chillingworth T., Connor R. Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., H. Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphi, Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G., "Deciphering the biology of Mycobacterium tuberculosis from complete genome sequence.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. STRAIN=CDC 1551 /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000030; M. Pfam; PF00823; PPE; 1. Hypothetical protein; (SEQUENCE 391 AA; 38)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      laboratory strains.";
Submitted (APR-2001) to the
EMBL; Z92539; CAB06873.1; -.
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356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMIL
VTGMMP-GMASAAKGTGAYAGPRYGFKPTVMP
                                                       MLGGLPVGQMGARAGGGLSGVLRVPPRPYVMP
                                                                                                                                               SSLGSSGLGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARRALPLTSLTSAAERGPGQ
                                                                                                                                                                                                                                                                                                                                                                  LEQAAAVEEASDTAAANQ-----LMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                 VATNVLGINTPAIMATEALYAEMWAQDALAMYGYAAASG-AAGMLQPLSPPSQTTNPGGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IATNLLGQNTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATATLLPFEEAPEMTSAGGL
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                                                                                                                                                                                                                        TPFVANIINSAVNTAAWYVNAAIPTAIFLANALNSGAPVAIAEGAIEAAEG---AASAAA
                                                                                                                                                                                                                                                                             P--ISMMVSMANNHMS-MTNSGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAMSSLG
                                                                                                                                                                                                                                                                                                                                    AAOSAAVGSAAATAAVNOVSVADLISSLPNAVSGLASPVTSVLDSTGLSGIIADIDALLA
                                                                                                         AGLADSVTPAGLGASLGEATLVGRLSVPAAWSTAAPATTAGATALEGSGWTVAAEEA-GP
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8081 MW; AFDF3EA4FB195C4F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 702; DB 16;
Pred. No. 1.4e-31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               n J.A., Carpenter L., White O
Gwinn M.L., Haft D., Hickey
L.A., Ermolaeva M.D., Salzbe
J., Khouri H., Gill J., Miku
386
                                                       385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           150;
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O06386;
01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-JUL-1997 (TrEMBLrel. 22, Last annotation update)
01-CCT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical 40.7 kDa protein (PPE family protein).
RV3621C OR MTCY15C10.31 OR MTCY07H7B.01 OR MT3723.

006386

413 AA

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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; Z95436; CAB08826.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AE007171; AAK48084.1; -. TIGR; MT3723; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey B., Rotonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula
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STRAIN=CDC 1551 / Oshkosh;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=98295987; PubMed=9634230;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mycobacterium tuberculosis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical
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Pfam; PF00823; PPE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Whole genome comparison of Mycobacterium tuberculosis clinical
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                   382
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   YVMPHSPAAG
                                                                                                                                                                                                                                                                                                            LIATNLLGQNTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATLLPFEEAPEMTSAGG
                                               WTATTPAASPAVLAASNGLGAAAAAEGSTHAFGGMPL--MGSGAGRAFNNFAAPRYGFKP
                                                                          WAAANQAVTPAARALPLTSLTSAAERGPGQMLGGLPVGQMGARAGGGLSGVL--RVPPRP
                                                                                                          YFGLAHDLPKWASEGAKAAGEAAKALPAAVPAIPSAGL-SGVAGAVGQAASVGGLKVPAV
                                                                                                                                                                     ALGLTGHTWSSDGSGLIVGGVLGDFVQGVTGSAELDASVAMDTFGKWVSPARLMVTQFKD
                                                                                                                                                                                                 MVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAA---AAQAVQT----
                                                                                                                                                                                                                              LASQAASVGQAVSGAANAQALTDIPKAL-----FGLSGIFTNEPPWLTDLGK
                                                                                                                                                                                                                                                            LLEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN
                                                                                                                                                                                                                                                                                          LLATNFLGQNTAAIAATEAQYAEMWAQDAAAMYGYAGASAAAT-QLSPFNPAAQTINPAG
                                                                                                                                                                                                                                                                                                                                                       SSAASMVAAATPQVAWLRSTAGQAEQAGSQAVAAASAYEAAFFATVPPPEIAANRALLMA
                                                                                                                                                                                                                                                                                                                                                                                   SSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI
                                                                                                                                                                                                                                                                                                                                                                                                                  MLDFAQLPPEVNSALMYAGPGSGPMLAAAAAWEALAAELQTTASTYDALITGLADGPWQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            al protein;
413 AA; 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      n; Complete proteome.
40679 MW; DAAFE8917A3900A3 CRC64;
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                                                                                                                                     AAQNGVRAMSSLGSSLGSSGLGGGVAANLGRAASVGSLSVPQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61;
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Best Local S
Matches 166
053958;
053958;
01-JUN-1998
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NCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E., Rolonay J.F., Nelson W.C., Umayam J.A., Ermolaeva M.D., Salzberg Kolonay J.F., Utterback T., Weidman J., Khouri H., Gill J., Mikula
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STRAIN=CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00823; PPE;
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InterPro; IPR000030; Microbac_PPE.
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Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 VDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                            LEQAAAVEEAS-----DTAAANQLMNNVPQALQQLA----QPTQ------
                                                                                                                                                                                                                                                                                                                                                                       IATNILGQNTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATATLLPFEEAPEMTSAGGL
                                                                                                                                                                                                                                                                                                                                                                                                                                   SAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMIL
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694 AA; 73206 M
                                                                                                                       AVTPAARALPLTSLTSA-AERGPGQMLGGLPVGQMGARAGGGL
                                                                                                                                                                                                                                                                                                                                                                                                                  SSAGMAAAAAPYVTWMSGTSAQAKAAADQARAAVVAYETAFAAVVPPPQIAANRSQLISL
                                                                                                                                                                                              AQAVQTAAQNGVRAMSSLGSSLG-----SSGLGGGVAANLGRAASVGSLSVPQAWAAANQ
                                                                                                                                                                                                                              IFGPTGATTYQNLFVTA----ANVTKFSTWANDAMSAPNLGMTEFKVF-----WQPPPA
                                                                                                                                                                                                                                                                                          AGQAAATGQATALASGTNAVTTALSSAAAQFPFDIIPTLLQGLATLSTQYTQLMGQLINA
                                                                                                                                                                                                                                                                                                                                                     VATNIFGQNTAAIAATEAEYGEMWAQDTMAMFGYASSSATA-SRLTPFTAPPQTTNPSGL
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                               PRELIMINARY;
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RESULT 14
P95190
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X Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
X Cole S.T., Brosch R., Parkhill J., Barry C.E. III, Tekaia F.,
X Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,
X Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
X Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
X Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
X Davies R., Devlin K., Krogh A., McLean J., Moule S., Murphy L.,
X Diver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
X A Rutter S., Seeger K., Krogh A., McLean J., Moule S.,
X Rajandream M.A., Rogers J.,
X Ra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local &
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               P95190;
P95190;
01-MAY-1997
01-MAY-1997
01-OCT-2002
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynobacterineae; Mycobacteriaceae; Mycobacterium.
Hypothetical
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01-MAR-2003
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PROSITE; PS00449; ATPASE_A; 1.
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                                                                                                                                                                                               TPAARALPLTSLTSA-AERGPGQMLGGLPVGQMGARAGGGL
                                                                                                                                                                                                                                                                                                                                                                                                   LEQAAAVEEAS------DTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGL-
                                                                                                                                                                                                                                                                                                                                                                                                                                    VATNIFGONTAAIAATEAEYGEMWAQDTMAMFGYASSSATA-SRLTPFTAPPQTTNPSGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                        IATNILIGQNTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATATILIPFEEAPEMTSAGGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SAGMAAAAAPYVTWMSGTSAQAKAAADQARAAVVAYETAFAAVVPPPQIAANRSQLISL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIGS
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                                                                                                                                                                  RLVANTLPATSLAAAPATQIPANLLGQMALGSM---TGGAL
                                                                                                                                                                                                                                                                     AVQTAAQNGVRAMSSLGSSLG-----
                                                                                                                                                                                                                                                                                                NAIFGPTGATTYONVFVTAANVTKFSTWANDAMSAPNLGMTEFKVF
                                                                                                                                                                                                                                                                                                                                                                    AGQAAATGQATALASGTNAVTTALSSAAAQFPFDIIPTLLQGLA--TLSTQYTQLMGQLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMIL
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(TrEMBLrel. 03, 0
(TrEMBLrel. 03, 1
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1 38.0 kDa protei
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                                                                                  PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                       WKTVSPHRSPISNMVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAAQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35.0%; Score 682.5; DB 16; Length 40.9%; Pred. No. 2.2e-30;
1. 03, Created)
1. 03, Last sequence update)
1. 22, Last annotation update)
protein (PPE family protein).
                                                                                                                                                                                                                                    - SSLGAGLGLRSGLSAGLAHAASAGLGQANLVGDLSVPPSWASATPAV
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Last
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                                                                                                                                                                                                                                                                   -SSGLGGGVAANLGRAASVGSLSVPQAWAAANQAV
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Best Local :
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MEDIINE=98295987; PubMed=9634230;
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Bavies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

STRAIN-CDC 1551 / Oshkosh;

Fleischmann R.D., Alland D., Eisen J.A., Carpenter

Fleischmann R.D., Alland D., Eisen J.A., Carpenter

Peterson J., DeBoy R., Dodson R., Gwinn M.L., Hatt

Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva

Belcher A., Utterback T., Weidman J., Khouri H., G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TIGR; MT3221; -.
TubercuList; Rv3136; -
InterPro; IPR000030; M:
Pfam; PF00823; PPE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (APR-2001) to the EMBL; Z83867; CAB06278.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Whole genome comparison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. STRAIN=H37RV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
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172; Conserv
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                                                                                                                                                                                                                                                                                                                               IATNILGONTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATATLIPFEEAPEMTSAGGI
                                                                                                                                                                                                                                                                      LEQAAAVEEASDTAAANQLMNNVPQALQQLAQPT---QGTTPSSKLGGLWKTVSPHRSPI
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MLGGLPVGQMGARAGGGLSGVL-RVPPRPYVMPHSPAAG
                                               GAASVGNTVLASVGRANSIGQLSVPPSWAAPSTRPVSALSPAGLTTLPGTDVAEHGMPG-
                                                                                         GSSGLGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSL--TSAAERG-PGQ
                                                                                                                                           SFVAGTIGAESNLGLLNVGDENPAEVTPGDFGIGELVSA----TSPGGGVSA-SGAG---
                                                                                                                                                                                        SNMVSM--ANNHMSMTNSGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAMSSLGSSL
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380 AA; 37979 MW;
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Pred. No. 4.4e-30;
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345B1EF9EC9AE4AA CRC64;
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H., Gill J.,
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Best Local S
Matches 161
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Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AL008967; CAA15564.1; ALT_INIT.
EMBL; AE007111; AAK47157.1; -.
TIGR; MT2838; -.
TIGR; MT2838; -.
Tuberculist; RV2768C; -.
InterPro; IPR000030; Microbac_PPE.
Pfam; PF00823; PPE; 1.
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C33310;
O1-JAN-1998 (TrEMBLrel. 05,
O1-MAR-2002 (TrEMBLrel. 20,
O1-OCT-2002 (TrEMBLrel. 22,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

STRAIN-CDC 1551 / Oshkosh;

Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,

Fleischmann R.D., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E.,

Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E.,

Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,

Belcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=98295987; PubMed=9634230; Garnier T., Churcher C., Harris D., Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Eiglmeier K., Gas S., Barry C.B. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Badcock K., Besham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G., "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PPE-family protein.
RV2768C OR MT2838 OR MTV002.33C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE 462 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Whole genome comparison of Mycobacterium tuberculosis clinical and
                                     308
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   292
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                                                                                                                                LEQAAAVEEASDTAAANQ-----LMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSP--H
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                                                                                                                                                                                                                                                                                                                           LGSSLGSSGLGG-GVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAERG 350
                                   ITFVQNAINGAVN----TTAWFVMATIPNAVFLGHAFAALNPATVTAAADAVPAAAAAAG
                                                                                                                                                                                                                                                     ASMSMVVAAQPYLAWLTYTAESAAHAAAQAMASAAAFEAAFAMTVPPAEVAANRALLAAL
                                                                       RSPISNMVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGV---RAMSS 291
                                                                                                             AGQAAAVSHAAAASTVQQVGLGSLISNLPNAVMGFASPLTSAADAAGLGGIIQDIEELLG
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Last annotation update)
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Search completed: November 21, 2003, 17:05:32 Job time: 43 secs

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Maximum Match 100%
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Maximum DB
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       GenCore version
Copyright (c) 1993 - 2003
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C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C;Accession: B70608
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Go
Connorr, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holr
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
Nature 
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C;Genetics:
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B70608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: DNA
A;Residues: 1-391 <COL>
A;Cross-references: GB:Z93777;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Gene:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary; nucleic acid sequence not shown; translation not shown
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PIDN:CAB07839.1; PID:e311073; I

Holroyd, S.; Gordon,

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genome

45	44	43	42	41	40	39	38	37	.36	35	34	33	32	31	30
409.5	412	412	414.5	415	415.5	418	418	422.5	423.5	426.5	428.5	429.5	439.5	441	443
21.0	21.1	21.1	21.3	21.3	21.3	21.4	21.4	21.7	21.7	21.9	22.0	22.0	22.6	22.6	22.7
409	645	590	987	582	618	3157	678	615	2523	443	1053	479	655	487	963
N	N	N	N	Ŋ	N	N	N	N	N	N	N	N	N	N	N
A70647	F70825	E70946	<b>E70808</b>	F70675	H70552	B70969	A70762	E70663	F70846	C70780	870987	D70676	A70931	C70830	B70524
probable PPE prote	e PPE	probable PPE prote		probable PPE prote				probable PPE prote	probable PPE prote	probable PPE prote	probable PPE prote	probable PE protei	O	probable PPE prote	probable PPE prote

## ALIGNMENTS

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probable PPE |
C;Specion
probable PPE protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C;Accession: C70568
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.;
CConnor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Ho
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A, Fitle: Deciphering the biology of Mycobacterium tuberculosis from the complete A;Recession: C70568
A;Accession: C70568
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
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A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete A;Reference number: A70500; MUID:98295987; PMID:9634230
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A;Cross-references: GB:Z75555; GB:AL123456; NID:g3261608;
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Mycobacterium tuberculosis
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                                                                                                                                                                                                                                                                                                                           GLPVGQMGARAG--GGLSGVLRVPPRPYVMPHSPAAG
                                                                                                                                                                                                                                                                                                                                                                             GSSGLGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAERGPGQMLG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LIATNILGONTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATATLLPFEEAPEMTSAGG
                                                                                                                                                                                                                                                                                                                                                         GSSGLGAGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAQTAPGHMLG
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                                                                                                                                                                                                                                                                                             GLPLGQLTNSGGGFGGVSNALRMPPRAYVMPRVPAAG
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Pred. No. 6.4e-91;
B; Mismatches 34;
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A; Experimental C; Genetics: A; Gene: PPE
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A; Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, A;Title: Deciphering the biology of Mycobacterium tuberculosis from the cc A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: G70929
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A;Residues: 1-393 <COL>
A;Cross-references: GB:Z95390; GB:AL123456;
A;Experimental source: strain H37Rv
C;Genetics:
A;Gene: PPE
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A; Cross-references: GB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          probable PPE protein - Mycobacterium tuberculosis (strain H37RV)

C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #text_change 22-Oct-1999
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C;Accession: G70929
C;Accession: G70929
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.;
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
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ASAAMAEAVAPYVAWMSAAAAQAEQAATQARAAAAAFEAAFAATVPPPLIAANRASLMQL
                           SAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMIL
                                                                                                                            VDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIGS
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                                                                                                                                                                                                40.0%; Score 779.5; DB 2
43.7%; Pred. No. 4.3e-39;
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81.5%; Pred. No. 1.4e
tive 20; Mismatches
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No. 1.
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L.4e-86;
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**AAEAPGALFGEMALSSLAGRALAGTAVRSGAGAARV** 

388

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probable PPE protein - Mycobacterium tuberculosis (strain H37RV)

()Species: Mycobacterium tuberculosis

()Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999

()Accession: A70932

R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Go.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holr.; Connor, R.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.; Rature 393, 537-544, 1998

A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete (A;Reference number: A70500; MUID:98295987; PMID:9634230

A;Accession: A70932

A;Status: preliminary; nucleic acid sequence not shown; translation not shown
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A;Residues: 1-409 <COL>
A;Cross-references: GB:AL022021; GB:AL123456; NID:g3250699; PIDN:CAA17729.1;
A;Experimental source: strain H37Rv
C;Genetics:
A;Gene: PPE
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177; Conserv
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                                                                                                                                                                                                                                                                                                                                                     IATNLLGQNTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATATLLPFEEAPENTSAGGL
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    AERGPGQMLGGLPVGQMGARAGGGL--
                                                                                                                                                                                                                                                                         LEQAAAVEEASDTAAA------NÇLMINIVPQALQQLAQPTQGTTPSSKLGGLWKTVSPH
                                                                                                                                                                                                                                                                                                                                                                                                              SSITMAAAVAPYVAWISVTAGQAEQAGAQAKIAAGVYETAFAATVPPPVIEANRALLMSL
                                                                                                                                                                                                                                                                                                                                                                                                                                               SAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPPVIAENRAELMIL
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                                             APLRGGYIGDITPLGGGATGGIARAIYVGSLSVPQGWAEAAPVMRAVASVLPGTGAAPAL
                                                                                       SSI-GSSLGS-SGLGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSA-
                                                                                                                                       LOSITTILANLTGPYSIIGLGAIPGGWWLTFGQILGLAQNAPGVAALLGPKAAAGALSPL
                                                                                                                                                                               RSPISNMVSMANNHMSMTNSGVS-----MTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAM
                                                                                                                                                                                                                                 AAQSAVVAQAAGAAASSDITAQLSQLISLLPSTLQSLA--TTATATSASAG--WDTV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TVSAAPEAAPGSLLGGLPL----AGAGGAGAGP-RYGFRPTVMARPPFAG 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GDAAKGLPGLGGMLG----GGPVAAGLGNAASVGKLSVPPVWSGPLPGSVTPGAAPLPVS
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R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, Comnor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
                                                                                     probable PPE protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change
C;Accession: B70931
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A;Residues: 1-403 <COL>
A;Cross-references: GB:AL022021; GB:AL123456; NID:g3250699; A;Experimental source: strain H37Rv C;Genetics:
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Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holr

Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.

Nature 393, 537-544, 1998

A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete

A;Reference number: A70500; MUID:98295987; PMID:9634230
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C;Species: Mycobacterium tuberculosis
C;Date: 17-U1-1998 #sequence_revision 17-Uu1-1998 #text_change 22-Oct-1999
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;Gene: PPE
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                                  SPAAG
                                                                    LGSALGGTPMVAPPPAVAAG----MPGMPFGTMGGQGFG-----RAVPQYGFRPNFVAR
                                                                                                        AARAL----PLTSLTSAAERGPGQMLGGLPVGQMGARAGGGLSGVLRVPP----RPYVMPH
                                                                                                                                                                  QTAAQNGVRAMSSIGSSI-----GSSGIGGGVAANIGRAASVGSISVPQAWAAANQAVTP
                                                                                                                                                                                                                    WLDKLWALLDPN-----
                                                                                                                                                                                                                                     KLGGLWKTVSPHRSPISNMVSMANNHMSMTNSGVSM-TNTLS---SMLKGFAPAAAAQAV
                                                                                                                                                                                                                                                                                          AAQSAAIAHATGASAGAQQTTLSQLIAAIPSVLQGLSSSTAATFASGPSGLLGIVGSGSS
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                                                                                                                                            LGEATSG-----GLGGALVAPLGSAGGLGGTVAAGLGNAATVGTLSVPPSWTAAAPLASP
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403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   37.8%;
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; Pred. No. 1.3e-36;
60; Mismatches 123;
                                                                                                                                                                                                                SNFWNTIASSGLFLPSNTIAPFLGLLGGVAAADAAGDV
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#text\_change 22-Oct-1999

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C;Species: Mycobacterium leprae
C;Date: 20-Apr-2001 #sequence_revision
C;Accession: H87056
R;Cole, S.T.; Eiglmeier, K.; Parkhill,
R.; Davies, R.M.; Devlin, K.; Duthoy, S
eam, M.A.; Rutherford, K.M.
                                                                                                                                                        Nature 409, 1007-1011, 2001
A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, N.;Aithers gene decay in the leprosy bacillus.
A;Reference number: A86909; MUID:21128732; PMID:11234002
A;Accession: H87056
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-421 <STO>
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A;Accession: B70931
A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
A;Residues: 1-423 <COL>
                                                                                                                    A;Cross-references:
C;Genetics:
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Matches 182
Query Match
Best Local Similarity
Matches 174; Conserv
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              37.5%;
nilarity 41.1%;
Conservative 5
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                                                                                                                                       GB:AL450380;
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                                                                                                                                     NID:g13093150;
            Score 731; DB 2;
Pred. No. 3.4e-36;
5; Mismatches 160
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Pred. No. 1.7e-36;
0; Mismatches 123
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S.; Feltwell, T.;
                                                                                                                                                                                                                                                                                                                                                                                                   20-Apr-2001 #text_change 20-Apr-2001
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                                                                                                                                       PIDN:CAC31563.1; GSPDB:GN00147
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                160;
                                                Length 421;
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              34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    probable PPE protein - Mycobacterium tuberculosis (strain H37RV)

C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C;Accession: G70925
C;Accession: G70925
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.;
C;Accession: R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; H,
Rajandream, M., Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 103 537-544 1088
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G70925
                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:Z74024; GB:AL123456;
A;Experimental source: strain H37Rv
C;Genetics:
A;Gene: PPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 393, 537-544, 1998
A;Authors: Sgares, R.; Sulston, J.E., Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: G70925
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Best Local S
Matches 182
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                                                                                                                                                                                                                                                                                                   182;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 SSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                1-408 <COL>
                                                                                                                                                                                                                                                                                                 Similarity 41.8
32; Conservative
                                                                                IATNILGQNTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATILPFEEAPEMTSAGGI
                                                                                                                                   AAASMVAAVTPYVÄMLSATAGQAEQAGMQARAAAAYELAFAMTVPPPVVVANRALLVAL
                                                                                                                                                                SAGLMVAAASPYVAMMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMIL 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAAQAVQTAAQNGVRAMSSLGSSLGSSGLGGGVAANLGRAASVGSLSVPQAWAAANQAVT
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            LEQAAA-----VEEASDTAAANQLMNN------VP--QALQQ-LAQPTQGTTPSSKL---
                                                    VATNFFGQNTPAIAATEAQYAEMWAQDAAAMYAYAGSAAIAT-ELTPFTAAPVTTSPAAL
                                                                                                                                                                                                                 MDFGVLPPEINSGRMYAGPGSGPMMAAAAAWDSLAAELGLAAGGYRLAISELTGAYWAGP
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                                                                                                                                                                                                                                                                                                 47;
                                                                                                                                                                                                                                                                                             Score 705; DB 2; I
Pred. No. 1.1e-34;
7; Mismatches 134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                           NID:g3250700;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      not shown; translation
                                                                                                                                                                                                                                                                                                                                       Length
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72;

Gaps

14;

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181 120

179

224

not

genome

PID:e1301025;

s, D.; Gordon, N.; Holroyd,

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332

358

272

214 179 180

298

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probable PPE protein - Mycobacterium tuberculosis (strain H37RV)
(;Species: Mycobacterium tuberculosis
(;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C;Accession: B70625
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Go; Connor, R.; Davles, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holr
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: B70625
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
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Best Local Similarity
Matches 166; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIGS 61
                                                                                   AGLADSVTPAGLGASLGEATLVGRLSVPAAWSTAAPATTAGATALEGSGWTVAAEEA-GP
                                                                                                                                                                                                                                                                                                LEQAAAVEEASDTAAANQ-----LMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MDFGALPPEINSARMYAGAGAGPMMAAGAAWNGLAAELGTTAASYESVITRLTTESWMGP
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          VTGMMP-GMASAAKGTGAYAGPRYGFKPTVMP
                                                                                                                              SSLGSSGLGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAERGPGQ 353
                                                                                                                                                                         TPFVANIINSAVNTAAWYVNAAIPTAIFLANALNSGAPVAIAEGAIEAAEG---AASAAA
                                                                                                                                                                                                              P--ISNMVSMANNHMS-MTNSGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAMSSLG
                                                                                                                                                                                                                                                         AAOSAAVGSAAATAAVNOVSVADLISSLPNAVSGLASPVTSVLDSTGLSGIIADIDALLA
                                                                                                                                                                                                                                                                                                                                        VATNVLGINTPAIMATEALYAEMWAQDALAMYGYAAASG-AAGMLQPLSPPSQTTNPGGL
                                                                                                                                                                                                                                                                                                                                                                                                                        ASMAMVAAAQPYLAWLTYTAEAAAHAGSQAMASAAAYEAAYAMTVPPEVVAANRALLAAL
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                                                 MLGGLPVGQMGARAGGGLSGVLRVPPRPYVMP 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VPPDWAARARWANPAAWRLPGDDVTALRGTAENA---LLRGFPMASAGOSTGGGF--VHK 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QAVQTAAQNGVRAMSSL--GSSLGS-----SGLGGGVAANLGRAASVGSLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----GGLWKTVSPHRSPISNMVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -GPRASPSVAGGGAVGGVQTPQPYWYWALDRESIGGSVSAALGKGSSAGSLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 702; DB 2;
Pred. No. 1.6e-34;
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            386
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R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998

A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
                                                                                                                                                                                                              RESULT
C70931
                                                                                                                          probable PPE protein - Mycobacterium tuberculosis (strain H37RV)
(;Species: Mycobacterium tuberculosis
(;Decies: Mycobacterium tuberculosis
(;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
(;Accession: C70931
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probable PPE protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C;Accession: F70560
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Go; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holr Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Tutle: Deciphering the biology of Mycobacterium tuberculosis from the complete A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: F70560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:Z95436; GB:AL123456; NID:g3261770; A;Experimental source: strain H37Rv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Status: preliminary; nucleic acid sequence not shown; translation A; Molecule type: DNA
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Best Local Similarity 39.1
Matches 168; Conservative
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TVIAQPPAGG
                                                     YVMPHSPAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LLEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN
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                                                                                                           WTATTPAASPAVLAASNGLGAAAAAEGSTHAFGGMPL--MGSGAGRAFNNFAAPRYGFKP
                                                                                                                                                             WAAANQAVTPAARALPLTSLTSAAERGPGQMLGGLPVGQMGARAGGGLSGVL--RVPPRP 381
                                                                                                                                                                                                                YFGLAHDLPKWASEGAKAAGEAAKALPAAVPAIPSAGL-SGVAGAVGQAASVGGLKVPAV
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                                                                                                                                                                                                                                                                                                                           ALGLTGHTWSSDGSGLIVGGVLGDFVQGVTGSAELDASVAMDTFGKWVSPARLMVTQFKD
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39.1%; Pred. No. 1.7e-34;
tive 61; Mismatches 145;
                                                                                                                                                                                                                                                                   -AAQNGVRAMSSLGSSLGSSGLGGGVAANLGRAASVGSLSVPQA 323
                                                                                                                                                                                                                                                                                                                                                                                                                                   ----FGLSGIFTNEPPWLTDLGK 226
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Holroyd, S.;
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genome

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probable PPE protein - Mycobacterium tuberculosis (strain H37RV)

C;Species: Mycobacterium tuberculosis

C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999

C;Accession: B70932

R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon

; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holröyd,

Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.

Nature 393, 537-544, 1998

A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A;Fitle: Deciphering the biology of Mycobacterium tuberculosis from the complete genor

A;Reference number: A70500; MUID:98295987; PMID:9634230

A;Accession: B70932

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Residues: 1-468 cOOL>

A;Experimental source: strain H37Rv

C:Genetics: Strain H37Rv

C:Genetics: Strain H37Rv
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B70932
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A;Accession: C70931
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-463 <COL>
A;Cross-references: GB:AL1022021; GB:AL123456; NID:g3250699; PIDN:CAA17723.1; PID:e125461
A;Experimental source: strain H37Rv
C;Genetics:
A;Gene: PPE
                                     S
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Best Local S
Matches 174
                                                                           Query Match
Best Local Similarity
Matches 164; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120 AATNIFGONTGAIAAAEARYAEMWAQDAAAMYGYAGSSSVAT-QVTPFAAPPPTTNAAGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      182 LEQAAAVEBASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVS--PHRSPI-
                               2 VDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 VDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIGS
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   MDFGLQPPEITSGEMYLGPGAGPMLAAAVAWDGLAAELQSMAASYASIVEGMASESWLGP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -SALGAGLGLRSAISSGLGSTAPAISAGASQAGSVGGMSVPPSWAAATPAIRTVAAVFSS
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                                                                                            35.0%;
40.9%;
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                                                                       Score 682.5; DB 2;
Pred. No. 2.8e-33;
9; Mismatches 125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 688.5; DB 2;
Pred. No. 1.2e-33;
8; Mismatches 136;
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Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the comple A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 probable PPE protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C;Accession: A70646
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: DNA
A;Residues: 1-380 <COL>
A;Cross-references: GB:Z83867; GB:AL123456;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 332 TPAARALPLTSLTSA-AERGPGQMLGGLPVGQMGARAGGGL 371
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 AAESMAVTAAPYIGWLYTTAEKTQQTAIQARAAALAFEQAYAMTLPPPVVVAANRIQLLAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 SAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMIL
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GSSGLGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSL--TSAAERG-PGQ
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                                                                                                  SFVAGTIGAESNLGLLNVGDENPAEVTPGDFGIGELVSA----TSPGGGVSA-SGAG---
                                                                                                                                                               SNMVSM--ANNHMSMTNSGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAMSSLGSSL
                                                                                                                                                                                                                                   TAQAAAVSQATDPLSL--LIETVTQALQALTIPSFIPEDFTFLDAIFAGYATVGVTQDVE
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Pred. No. 6.1e-33;
6; Mismatches 143
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R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:98295987; PMID:9634230
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C;Accession: G70881
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C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
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G70881
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A;Residues: 1-394 <COL>
A;Cross-references: GB:AL008967; GB:AL123456; NID:g3261491; PIDN:CAA15564.1; PID:e117389
A;Experimental source: strain H37Rv
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Search completed: November 21, 2003, 17:06:04 Job time : 21 secs
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A;Status: preliminary; nucleic acid sequence not shown; translation not shown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 182 LEQAAAVEEASDTAAANQ-----LMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSP--H 234
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                                                                                                                                                                                                                                                                                                              240 ITFVQNAINGAVN----TTAWFVMATIPNAVFLGHAFAALNPATVTAAADAVPAAAAAG 295
                                                                                                                                                                                                                                                                                                                                                              235 RSPISNMVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGV---RAMSS 291
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                                                                                                                                                   PGQMLGGLPVGQMGARAGGGLSGVLRVPPRPYVMP 385
                                                                                                                                                                                                           LAHTVTPVGVGGASLTASLGEASSVGGLSVPAGWSTAAPAWTSGTTALEGSGWAVPEEAG
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